

Europäisches Patentamt
European Patent Office
Office européen des brevets



(11) **EP 0 864 585 A1**

(12) **EUROPEAN PATENT APPLICATION**

(43) Date of publication:
16.09.1998 Bulletin 1998/38

(51) Int. Cl.⁶: **C07K 14/715, A61K 38/17,
A61K 39/00**

(21) Application number: 97310517.4

(22) Date of filing: 23.12.1997

(84) Designated Contracting States:
**AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC
NL PT SE**
Designated Extension States:
AL LT LV MK RO SI

(30) Priority: 12.03.1997 JP 74697/97
28.07.1997 JP 215488/97
09.10.1997 JP 291837/97

(71) Applicant:
**KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU
KAGAKU KENKYUJO
Okayama-shi Okayama (JP)**

(72) Inventors:
• Torigoe, Kakuji
Kurashiki-shi, Okayama (JP)
• Okura, Takanori
Kurashiki-shi, Okayama (JP)
• Kurimoto, Masashi
Okayama-shi, Okayama (JP)

(74) Representative:
**Daniels, Jeffrey Nicholas et al
Page White & Farrer
54 Doughty Street
London WC1N 2LS (GB)**

Remarks:
The applicant has subsequently filed a sequence listing and declared, that it includes no new matter.

(54) **Interleukin-18-receptor proteins**

(57) Disclosed are a polypeptide (including that in soluble form) as receptor for a novel cytokine, i.e., interleukin-18, a DNA encoding the polypeptide, and the uses of the polypeptide including pharmaceutical and neutralizer to interleukin-18. Pharmaceuticals with the polypeptide is useful to treat and prevent autoimmune and allergic disease because it suppresses and regulates excessive immunoreaction.

EP 0 864 585 A1

Description**Background of the Invention**5 **1. Field of the Invention**

This invention relates to a novel receptor protein which recognizes a cytokine, more particularly, to a novel polypeptide which recognizes interleukin-18 (hereinafter abbreviated as "IL-18").

10 **2. Description of the Prior Art**

IL-18 is a type of cytokine or substance which mediates signal transduction in immune system. As seen in Japanese Patent Kokai Nos.27,189/96 and 193,098/96 and Haruki Okamura et al., *Nature*, Vol.378, No.6,552, pp.88-91 (1995), IL-18 was provisionally designated as "interferon-gamma inducing factor" immediately after its discovery: This designation was changed later into "IL-18" in accordance with the proposal in Shimpei Ushio et al., *The Journal of Immunology*, Vol.156, pp.4,274-4,279 (1996). IL-18 in mature form consists of 157 amino acids and possesses properties of inducing in immunocompetent cells the production of interferon-gamma (hereinafter abbreviated as "IFN- γ ") which is known as useful biologically-active protein, as well as of inducing and enhancing the generation and cytotoxicity of killer cells. Energetic studies are now in progress to develop and realize various uses of IL-18 in pharmaceuticals such as antiviral, antimicrobial, antitumor and anti-immunopathic agents which have been in great expectation because of these properties of IL-18.

As described above, in nature, cytokines including IL-18 are produced and secreted as substances responsible for signal transduction in immune system. Therefore, excessive amounts of cytokines may disturb the equilibria in immune system when they are produced or administered in the body of mammals. The surface of usual mammalian cells may bear certain sites or "receptors" which are responsible for recognition of cytokines: Secreted cytokines transduce no signal in cells till they are bound to the receptors. In normal immune system, there would be definite equilibria between respective cytokines and their receptors. Thus, in this field, with the purpose of developing and realizing IL-18 as pharmaceuticals, in addition to the clarification of physiological activities of IL-18, an expedited establishment of mass production and characterization of IL-18 receptor (hereinafter abbreviated as "IL-18R") have been in great expectation.

30 **Summary of the Invention**

In view of the foregoing, the first object of this invention is to provide a polypeptide as IL-18R which can be easily prepared on a large scale.

35 The second object of this invention is to provide uses of such polypeptide as pharmaceuticals.

The third object of this invention is to provide a DNA which encodes the polypeptide.

The fourth object of this invention is to provide a process to prepare the polypeptide.

The fifth object of this invention is to provide an agent to neutralize IL-18 using the polypeptide.

40 The sixth object of this invention is to provide a method to neutralize IL-18 using the polypeptide.

We energetically and extensively screened various means which might attain these objects, eventually resulting in the finding that a substance which recognized IL-18 was present in L428 cell, a type of lymphoblastoid cell derived from a patient with Hodgkin's disease. We isolated and characterized this substance, revealing that its nature was proteinaceous, as well as that it well recognized and bound IL-18 even when in isolated form. It was also found that the IL-18R thus identified was efficacious in treatment and prevention of various diseases resulting from excessive immunoreaction, such as autoimmune diseases, because in mammals including human, IL-18R recognized and neutralized IL-18 which activated immune system. Further, we have energetically studied L428 cell using as probe some partial amino acid sequences of the IL-18R, resulting in obtainment of a DNA which did encode IL-18R. We confirmed that a polypeptide obtained by bringing such DNAs into expression in artificial manner well recognized IL-18 and shared some essential physiological activities with the IL-18R separated from L428 cell, as well as that it was preparable in desired amounts by recombinant DNA techniques using such DNA. Thus we accomplished this invention.

50 More particularly, this invention attains the first object with a polypeptide as IL-18R, which is obtainable through gene expression.

This invention attains the second object with an agent for IL-18R susceptible diseases, which contains as effective ingredient such polypeptide.

55 This invention attains the third object with a DNA which encodes the polypeptide.

This invention attains the forth object with a process to prepare polypeptide, comprising bringing into expression a DNA which encodes the polypeptide, and collecting the resultant polypeptide.

This invention attains the fifth object with an agent to neutralize IL-18, which contains as effective ingredient the

polypeptide.

This invention attains the sixth object with a method to neutralize IL-18, characterized by allowing the polypeptide to act on IL-18.

L428 cell, which is feasible in this invention, have been deposited in the Patent Microorganism Depository, National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology, 1-3, Higashi 1 chome, Tsukuba-shi, Ibaraki-ken, 305, Japan, under the accession number of "FERM BP-5777" on and after December 24th, 1996.

Brief Explanation of the Accompanying Drawings

FIG. 1 shows that the monoclonal antibody MAb #117-10C binds to L428 cells and IL-18R while competing with IL-18.

FIG. 2 is an image of intermediate tone given on display, which shows IL-18R on gel electrophoresis visualized by the Western blotting method using the monoclonal antibody MAb #117-10C.

FIG. 3 shows the inhibitory action of the monoclonal antibody MAb #117-10C on the activity of IL-18.

FIG. 4 is the chromatogram obtained by applying to IL-18R an immunoaffinity chromatography using the monoclonal antibody MAb #117-10C.

FIG. 5 is the peptide map of IL-18R.

FIG. 6 shows the structure of the recombinant DNA "pcDNA/HuIL-18R" of this invention.

FIG. 7 shows the structure of the recombinant DNA "pEFHIL18R-14" of this invention.

FIG. 8 shows the structure of the recombinant DNA "pEFHIL18RD1-2-H" of this invention.

FIG. 9 shows the structure of the recombinant DNA "pEFHIL18RD1-H" of this invention.

FIG. 10 shows the structure of the recombinant DNA "pEFMIL18RSHT" of this invention.

Throughout the Figures, the symbol "Pcmv" indicates the cytomegalo virus promotor; "EF1 α P", the elongation factor promotor; "IL-18R cDNA", the cDNA encoding the polypeptide of this invention; "EFHIL18R-14 cDNA", the cDNA encoding the soluble polypeptide of human origin according to this invention; "HIL18RD1-2-H cDNA", the cDNA encoding the soluble polypeptide of human origin according to this invention; "HIL18RD1-H cDNA", the cDNA encoding the soluble polypeptide of human origin according to this invention; and "EFMIL18RSHT cDNA", the cDNA encoding the soluble polypeptide of mouse origin according to this invention.

Detailed Description of the Invention

This invention relates to a polypeptide as IL-18R, which is obtainable through gene expression. The polypeptide of human origin according to this invention usually contains as partial amino acid sequence(s) one or more amino acid sequences of SEQ ID NOs:12 to 19: As a whole, it contains a part or whole of the amino acid sequence of SEQ ID NO: 20. While the polypeptide of mouse origin according to this invention usually contains a part or whole of the amino acid sequence of SEQ ID NO:21. Thus, the wording "polypeptide" as referred to in this invention shall include, in addition to those which wholly contain the amino acid sequence of either SEQ ID NO:20 or 21, for example, those which contain the same amino acid sequence but with addition of one or more amino acids, in particular, those which contain one or more amino acids linked to the C-and/or N-termini in SEQ ID NO:20 or 21; those which contain the same amino acid sequence as in SEQ ID NOs:20 and 21 but with deletion of one or more amino acids, in particular, soluble polypeptides which contain the amino acid sequences of SEQ ID NOs:22 to 25; and those which contain either of the amino acid sequences as described above but with a saccharide chain, as far as they are obtainable through gene expression and possess the essential functions of IL-18R. As to IL-18, those of human and mouse origins commonly consisting of 157 amino acids have been documented: Human IL-18 bears the amino acid sequence of SEQ ID NO:26 (where the amino acid with symbol "Xaa" represents either isoleucine or threonine), while mouse counterpart, the amino acid sequence of SEQ ID NO:27 (where the amino acid with symbol "Xaa" represents either methionine or threonine).

The polypeptide of this invention is usually prepared by applying recombinant DNA techniques, more particularly, by bringing into expression in artificial manner a DNA which encodes the polypeptide, and collecting the resultant polypeptide. This invention provides, in addition to a DNA which encodes the polypeptide, a process to prepare the polypeptide using recombinant DNA techniques: By practicing such a process according to this invention, desired amounts the polypeptide can be easily obtained.

The DNA which is used in this invention are those which originating natural sources, those which can be obtained by artificially modifying them and those which can be obtained through chemical synthesis, provided that they do encode the polypeptide. Generally, in this field, in case of artificially expressing DNAs which encode polypeptides, one may replace one or more nucleotides in the DNAs with different nucleotides and/or link an appropriate nucleotide sequence to the DNAs, with purpose of improving their expression efficiency and/or the physiological and physico-chemical properties of the polypeptides. Such modifications are feasible in the DNA of this invention of course: For

example, one can link to the 5'-and 3'-termini of the DNA as described above recognition sites for appropriate restriction enzymes, initiation and termination codons, promoters and/or enhancers, as far as the final polypeptide products do retain desired physiological activities. Thus, the wording "DNA" as referred to in this invention shall mean, in addition to those which encode any polypeptides as described above, those which are complementary thereto, and further those where one or more nucleotides have been replaced with different nucleotides while conserving the amino acid sequence.

To obtain such a DNA from natural sources, for example, mammalian cells including epithelial cells, endothelial cells, interstitial cells, chondrocytes, monocytes, granulocytes, lymphocytes neurocytes and their established cell lined of human and mouse origins are screened with oligonucleotides as probe which can be prepared with reference to the amino acid sequences of SEQ ID NOs:12 to 25. Examples of preferred cells are cell lines which are obtained by establishing hemopoietic cells including lymphocytes, in particular, JM cells, HDLM-2 cells, MOLT-16 cells and PEER cells described in Jun Minowada, *Cancer Review*, Vol.10, pp.1-18 (1988), and lymphoblastoid cells such as L428 cell (FERM BP-5777), KG-1 cell (ATCC CCL-246) and U-937 cells (ATCC CRL-1593.2). The human and mouse DNAs obtained in this way usually contain a part or whole of respective nucleotide sequences of SEQ ID NOs:1 and 2. For example, as shown in SEQ ID NO:7, the DNA obtained from L428 cell, a type of lymphoblastoid cell derived from a patient with Hodgkin's disease, consists of the nucleotide sequence of SEQ ID NO:1 encoding the amino acid sequence of SEQ ID NO:20, and another nucleotide sequence encoding signal peptide which is linked to the 5'-terminal in the nucleotide sequence of the SEQ ID NO:1. Soluble polypeptides with the amino acid sequences of SEQ ID NOs:22 to 25 are usually encoded by respective nucleotide sequences of SEQ ID NOs:3 to 6, which are usually used in a form where, as shown in the nucleotide sequences of SEQ ID NOs:8 to 11, a nucleotide sequence encoding signal peptide is linked to the 5'-terminal in the nucleotide sequences of SEQ ID NOs:3 to 6. Such a DNA can be also obtained through usual chemical synthesis, and in any case, DNAs can be amplified to desired levels by PCR method once they become available. By the way, the amino acid sequences of SEQ ID NOs:20 and 21 are described along with the amino acid sequences for signal peptides in P. Parnet et al., *The Journal of Biological Chemistry*, Vol.271, pp.3,967-3,970 (1996): This paper however makes neither suggestion nor teaching that the polypeptides with the amino acid sequences of SEQ ID NOs:20 and 21 do function as IL-18R.

Such DNA expresses the polypeptide when introduced into an appropriate host of microbe, animal or plant origin. The DNA of this invention is usually prepared into a recombinant DNA prior to introduction into host. Such recombinant DNA, which consists of the DNA of this invention and an autonomously replicable vector, can be easily prepared with usual recombinant DNA techniques, provided that the DNA is available. Examples of vectors which can receive the DNA of this invention are plasmid vectors including pKK223-3, pCDNA1/Amp, BCMGSNeo, pcDL-SR α , pKY4, pCDM8, pCEV4, pME18S and pEF-BOS. Autonomously replicable vectors usually comprises other nucleotide sequences, for example, promoter, enhancer, replication origin, terminator of transcription, splicing sequence and/or selection marker which facilitate the expression of the DNA of this invention in particular hosts. Expression of the DNA becomes artificially regulatable upon external stimuli when it is used in combination with either heat shock protein promoter or interferon- α promoter as disclosed in Japanese Patent Kokai No. 163,368/95 by the same applicant.

Conventional methods are feasible in the insertion of the DNA of this invention into such vector. More particularly, a gene with the DNA of this invention and an autonomously replicable vector are first digested with restriction enzyme and/or ultrasonication, then the resultant DNA and vector fragments are ligated. Ligation of DNA and vector fragments become much easier when genes and vectors are digested with restriction enzymes specific to particular nucleotides, for example, *AccI*, *BamHI*, *BstXI*, *EcoRI*, *HindIII*, *NotI*, *PstI*, *SacI*, *Sall*, *SmaI*, *SpeI*, *XbaI* and *XhoI*. To ligate DNA and vector fragments, they are first annealed, if necessary, then exposed to DNA ligase *in vivo* or *in vitro*. The recombinant DNA thus obtained is unlimitedly replicable in hosts of microbe and animal origins.

Such recombinant DNA is introduced into an appropriate host, prior to use in preparation of the polypeptide. Although conventional hosts of microbe, animal and plant origins are feasible in this invention, it is preferable to choose a host of yeast or mammalian origin in case that the final use of the polypeptide is pharmaceuticals. Examples of host cells of mammalian origin are epithelial cell, interstitial cell and hemopoietic cell of human, monkey, mouse and hamster origins, in particular, 3T3 cell (ATCC CCL-92), C127I cell (ATCC CRL-1616), CHO-K1 cell (ATCC CCL-61), CV-1 cell (ATCC CCL-70), COS-1 cell (ATCC CRL-1650), HeLa cell (ATCC CCL-2), MOP-8 cell (ATCC CRL-1709) and their mutant strains. To introduce the DNA of this invention into such a host, one can employ conventional methods, for example, DEAE-dextran method, calcium phosphate transfection method, electroporation method, lipofection method, micro-injection method and viral infection method using retrovirus, adenovirus, herpesvirus and vaccinia virus. To select among the resultant transformants a clone which is capable of producing the polypeptide, the transformants are cultivated on culture medium, followed by selecting one or more clones where production of the polypeptide is observed. Recombinant DNA techniques using host cells of mammalian origin are detailed, for example, *Jikken-Igaku-Bessatsu*, *Saibo-Kogaku Handbook* (The handbook for the cell engineering), edited by Toshio KUROKI, Masaru TANIGUCHI and Mitsuo OSHIMURA, published by Yodosha. Co., Ltd., Tokyo, Japan (1992), and *Jikken-Igaku-Bessatsu*, *Biomanual Series 3, Idenshi-Cloning-Jikken-Ho* (The experimental methods for the gene cloning), edited by Takashi YOKOTA and

Kenichi ARAI, published by Yodosha Co., Ltd., Tokyo, Japan (1993).

The transformant thus obtained produces and secretes the polypeptide inside and/or outside the host cell when cultivated on culture medium. Such cultivation is feasible with conventional culture media directed to cultivation of transformants, which are usually composed by adding to a bufferized water as base inorganic ions such as sodium ion, potassium ion, calcium ion, phosphoric ion and chloric ion; minor elements, carbon sources, nitrogen sources, amino acids and vitamins which meet to the metabolism of particular hosts; and, if necessary, sera, hormones, cell growth factors and cell adhesion factors. Particular media are, for example, 199 medium, DMEM medium, Ham's F12 medium, IMDM medium, MCDB 104 medium, MCDB 153 medium, MEM medium, RD medium, RITC 80-7 medium, RPMI-1630 medium, RPMI-1640 medium and WAJC 404 medium. One can obtain a culture product containing the polypeptide by inoculating on such a culture medium a transformant in an amount of 1×10^4 - 1×10^7 cells/ml, preferably, 1×10^5 - 1×10^6 cells/ml, and subjecting the transformant to suspension or monolayer culture at around 37°C for 1 day to 1 week, preferably, 2 to 4 days while replacing the culture medium with a fresh preparation, if necessary. The culture product thus obtained usually contains about 1 µg/l to 1 mg/l polypeptide, dependently of the type of transformant and cultivation conditions.

The culture product obtained in this way is first subjected to ultrasonication, cell-lytic enzyme and/or detergent to disrupt cells, if necessary, then polypeptides are separated from the cells or cell debris by filtration and centrifugation, followed by purification. In the purification, a culture product which has been separated from cell or cell debris is subjected to conventional methods common in purification of biologically-active proteins, for example, salting-out, dialysis, filtration, concentration, fractional precipitation, ion-exchange chromatography, gel filtration chromatography, adsorption chromatography, isoelectric focusing chromatography, hydrophobic chromatography, reversed phase chromatography, affinity chromatography, gel electrophoresis and isoelectric focusing gel electrophoresis which are used in combination, if necessary. The purified polypeptide is then concentrated and lyophilized into liquid or solid to meet to its final use. The IL-18 and monoclonal antibody, disclosed in Japanese Patent Kokai No.193,098/96 and Japanese Patent Application No.356,426/96 by the same applicant, are very useful in purification of the polypeptide: Immunoaffinity chromatographies using these do yield a high-purity preparation of the polypeptide with minimized costs and labors.

The polypeptide of this invention exhibits a remarkable efficacy in treatment and prevention of various diseases resulting from excessive immunoreaction because in mammals including human, the polypeptide recognizes and binds IL-18 which may activate immune system. Immune system, which is in nature to defend living bodies from harmful foreign substances, may cause unfavorable results in living bodies because of its nature. When mammals receive a graft of organ, for example, skin, kidney, liver, heart and bone marrow, the rejection reaction and immunoreaction against alloantigen may activate T-cells, resulting in the occurrence of inflammation and proliferation of lymphocytes. Similar phenomena are observed in case that host receives the invasion by heteroantigens, for example, allergens, which are not recognized as self. In autoimmune diseases, allergic reactions are induced by substances which must be recognized as self. The polypeptide of this invention exhibits a remarkable efficacy in treatment and prevention of various diseases resulting from such an immunoreaction because the polypeptide suppresses or regulates the immunoreaction when administered in mammals including human. Thus, the wording "susceptive diseases" as referred to in this invention shall mean all the diseases resulting from augmented immunoreaction which can be treated and/or prevented by the direct or indirect action of IL-18R: Particular susceptible diseases are, for example, rejection reactions associated with a graft of organ as described above, autoimmune and allergic diseases including pernicious anemia, atrophic gastritis, insulin-resistant diabetes, Wegener granulomatosis, discoid lupus erythematosus, ulcerative colitis, cold agglutinin-relating diseases, Goodpasture's syndrome, primary biliary cirrhosis, sympathetic ophtalmitis, hyperthyroidism, juvenile onset type diabetes, Sjögren syndrome, autoimmune hepatitis, autoimmune hemolytic anemia, myasthenia gravis, systemic scleroderma, systemic lupus erythematosus, polyleptic cold hemoglobinuria, polymyositis, periarteritis nodosa, multiple sclerosis, Addison's disease, purpura hemorrhagica, Basedow's disease, leukopenia, Behçet's disease, dimacterium praecox, rheumatoid arthritis, rheumatopyra, chronic thyroiditis, Hodgkin's disease, HIV-infections, asthma, atopic dermatitis, allergic nasitis, pollinosis and apitoxin-allergy. In addition, the polypeptide of this invention is efficacious in treatment and prevention of septic shock which results from production or administration of excessive IFN-γ.

Thus, the agent for susceptible disease, which contains as effective ingredient the polypeptides of this invention, would find a variety of uses as anti-autoimmune-diseases, anti-allergies, anti-inflammatories, immunosuppressants, hematopoietics, leukopoietics, thrombopoietics, analgesics and antipyretics directed to treatment and/or prevention of susceptible diseases as illustrated in the above. The agent according to this invention is usually prepared into liquid, suspension, paste and solid forms which contain the polypeptide in an amount of 0.00001-100 w/w %, preferably, 0.0001-20 w/w %, dependently on the forms of agents as well as on the types and symptoms of susceptible disease.

The agent for susceptible diseases according to this invention includes those which are solely composed of the polypeptide, as well as including those in composition with, for example, one or more physiologically-acceptable carriers, excipients, diluents, adjuvants, stabilizers and, if necessary, other biologically-active substances: Examples of such stabilizer are proteins such as serum albumins and gelatin; saccharides such as glucose, sucrose, lactose, maltose,

trehalose, sorbitol, maltitol, mannitol and lactitol; and buffers which are mainly composed of phosphate or succinate. Examples of the biologically-active substances usable in combination are FK506, glucocorticoid, cyclophosphamide, nitrogen mustard, triethylenethiophosphoramide, busulfan, pheniramine mustard, chlorambucil, azathioprine, 6-mercaptopurine, 6-thioguanine, 6-azaguanine, 8-azaguanine, 5-fluorouracil, cytarabine, methotrexate, aminopterin, mitomycin C, daunorubicin hydrochloride, actinomycin D, chromomycin A₃, bleomycin hydrochloride, doxorubicin hydrochloride, cyclosporin A, L-asparaginase, vincristine, vinblastine, hydroxyurea, procarbazine hydrochloride, adrenocortical hormone and auri colloid; receptor antagonists to cytokines other than IL-18, for example, antibodies respectively against interleukin-1 receptor protein, interleukin-2 receptor protein, interleukin-5 receptor protein, interleukin-6 receptor protein, interleukin-8 receptor protein and interleukin-12 receptor protein; and antagonists respectively against TNF- α receptor, TNF- β receptor, interleukin-1 receptor, interleukin-5 receptor and interleukin-8 receptor.

The agent for susceptible diseases according to this invention includes pharmaceuticals in minimal dose unit: The wording "pharmaceutical in minimal dose unit" represents those which are prepared into a physically united form suitable for prescription and also allowed to contain the polypeptide in an amount corresponding to its single dose or multiple (up to 4-fold) or divisor (up to 1/40) thereof: Examples of such form are injection, liquid, powder, granule, tablet, capsule, sublingual, ophthalmic solution, nasal drop and suppository. The agent for susceptible diseases according to this invention can be administrated through both oral and parenteral routes to exhibit in each case a remarkable efficacy in treatment and prevention of susceptible diseases. More particularly, the polypeptide is administered through oral route or parenteral route such as intradermal, subcutaneous, intramuscular or intravenous route at a dose of about 1 μ g/time/adult to about 1g/time/adult, preferably, about 10 μ g/time/adult to about 100 mg/time/adult 1 to 4 times/day or 1 to 5 times/week over 1 day to 1 year.

The DNA which encodes the polypeptide of this invention is useful in "gene therapies". Particularly, in usual gene therapies, the DNA of this invention is first inserted in a vector derived from virus such as retrovirus, adenovirus or adeno-associated virus and, alternatively, embedded in either cationic- or membrane fusible-liposomes, then the inserted or embedded DNA is directly injected in a patient with an IL-18 susceptible disease and, alternatively, introduced into lymphocytes, which have been collected from the patient, and implanted in the patient. In adoptive immune gene therapies, by introducing the DNA of this invention into effector cells similarly as in the usual gene therapies, the cytotoxicity of effector cells against tumors and virus-infected cells is enhanced and this would strengthen adoptive immunotherapy. In tumor vaccine gene therapy, tumor cells, which have been extracted from a patient, are introduced with the DNA of this invention similarly as in the usual gene therapies, allowed to proliferate in vitro to a prescribed level and then self-transplanted to the patient: The transplanted tumor cells act as vaccine in the body of the patient, exhibiting a strong and antigen-specific antitumor immunity. Thus, the DNA of this invention exhibits a remarkable efficacy in gene therapies for various diseases including, for example, malignant tumors, viral diseases, infections and autoimmune diseases, as well as in suppression of rejection reaction and excessive immunoreaction associated with grafts of organs and allergic diseases. General procedures for gene therapies are detailed in *Jikken-Igaku-Bessatsu, Biomanual UP Series, Idenshichiryō-no-Kisogijutsu* (Basic techniques for the gene therapy), edited by Takashi SHIMADA, Izumi SAITO, and Keiya OZAWA, published by Yodosha Co., Ltd., Tokyo, Japan (1996).

Further, the polypeptide of this invention is useful in affinity chromatography and labelled assay directed to purification and detection of IL-18 because the polypeptide bears properties of recognizing and binding IL-18. In addition, the polypeptide of this invention, in particular, that in soluble form is useful in screening *in vivo* or *in vitro* agonists and antagonists to IL-18. Furthermore, the agent to neutralize IL-18 containing as effective ingredient the polypeptide and the method to neutralize IL-18 where IL-18 is exposed to the polypeptide are useful in treatment of various diseases which result from production and administration of excessive IL-18.

The following Examples are to illustrate the way of practicing this invention. The techniques employed in Examples 1 to 3 are common in this field as detailed, for example, *Jikken-Igaku-Bessatsu, Saibo-Kogaku Handbook* (The handbook for the cell engineering), edited by Toshio KUROKI, Masaru TANIGUCHI and Mitsuo OSHIMURA, published by Yodosha Co., Ltd., Tokyo, Japan (1992), and *Jikken-Igaku-Bessatsu, Biomanual Series 3, Idenshi-Cloning-Jikken-Ho* (The experimental methods for the gene cloning), edited by Takashi YOKOTA and Kenichi ARAI, published by Yodosha Co., Ltd., Tokyo, Japan (1993).

50 Example 1

Preparation and characterization of IL-18R

Example 1-1

Preparation of IL-18R

Newborn hamsters were intraperitoneally injected with an anti-lymphocyte antibody of rabbit origin to suppress

their possible immunoreaction, subcutaneously injected at their dorsal areas with about 5×10^5 cell/animal of L428 cells (FERM BP-5777), a type of lymphoblastoid cell derived from a patient with Hodgkin's disease, and fed in usual manner for 3 weeks. The tumor masses, subcutaneously occurred, about 10g each, were extracted, disaggregated and washed in usual manner in serum-free RPMI-1640 medium (pH 7.4), thus obtaining proliferated cells.

The proliferated cells were added with a mixture solution (volume ratio of 9:1) of 0.83 w/v % NH_4Cl and 170mM Tris-HCl buffer (pH 7.7) in an amount 10-fold larger than the wet weight of the cells, stirred and collected by centrifugation at 2,000rpm for 10 minutes. The cells were then suspended in an appropriate amount of phosphate buffered saline (hereinafter abbreviated as "PBS"), stirred, collected by centrifugation at 2,000rpm, resuspended to give a cell density of about 1×10^8 cells/ml in 10mM Tris-HCl buffer (pH 7.2) with 1mM MgCl_2 and disrupted with "POLYTRON", a cell disrupter commercialized by Kinematica AG, Littau/Lucerne, Switzerland. The resultant was added with 10mM Tris-HCl buffer (pH 7.2) containing both 1mM MgCl_2 and 1M sucrose to give a final sucrose concentration of 0.2M, and centrifuged at 1,000rpm to collect the supernatant which was then centrifuged at 25,000rpm for 60 minutes, followed by collecting the precipitate. The precipitate was added with adequate amounts of 12mM 3-[(3-cholamidopropyl)dimethylammonio]-1-propanesulfonic acid (hereinafter abbreviated as "CHAPS"), 10mM ethylenediaminetetraacetic acid (hereinafter abbreviated as "EDTA") and 1mM phenylmethylsulfonylfluoride, stirred at 4°C for 16 hours, and centrifuged at 25,000rpm for 60 min, followed by collecting the supernatant.

The supernatant was charged to a column of "WHEAT GERM LECTIN SEPHAROSE 6B", a gel product for affinity chromatography commercialized by Pharmacia LKB Biotechnology AB, Uppsala, Sweden, pre-equilibrated in PBS with 12mM CHAPS, and the column was washed with PBS containing 12mM CHAPS, and then charged with PBS containing both 0.5 M N-acetyl-D-glucosamine and 12mM CHAPS while monitoring the protein content in the eluate with the absorbance of ultraviolet at a wave length of 280nm. The fractions with an absorbance of 0.16-0.20 were collected and pooled, thus obtaining about 25 liters of aqueous solution with a protein content of about 1 mg/ml per 10^{12} starting cells.

A small portion of the solution was sampled, added with 4ng human IL-18 which had been ^{125}I -labelled in usual manner, incubated at 4°C for 1 hour, added with appropriate amounts of "POLYETHYLENE GLYCOL 6000", a polyethylene glycol preparation with an averaged molecular weight of 6,000 daltons, commercialized by E. Merck, Postfach, Germany, and allowed to stand under ice-chilling conditions for 30 minutes to effect binding reaction. The reaction product was centrifuged at 6,000rpm for 5 minutes and the resultant precipitate was collected to determine the level of radioactivity. In parallel, there was provided another sections as control in which 3μg non-labelled human IL-18 was used along with ^{125}I -labelled human IL-18 and treated similarly as above. Comparison with control revealed that the radioactivity of the precipitate from the sample solution was significantly higher. This indicated that the aqueous solution obtained in the above did contain IL-18R and the IL-18R recognized and bound IL-18 when exposed to IL-18.

Example 1-2

Binding ability to monoclonal antibody

L428 cells (FERM BP-5777) were suspended in RPMI-1640 medium (pH7.4), supplemented with 0.1 v/v % bovine serum albumin and also containing 0.1 v/v % NaN_3 , to give a cell density of 4×10^7 cells/ml, while monoclonal antibody MAb#117-10C specific to human IL-18R, obtained by the method described in Japanese Patent Application No.356,426/96 by the same applicant, was dissolved in another preparation of RPMI-1640 medium supplemented with 0.1 w/v% bovine serum albumin to give different concentrations of 0.019 μg/ml, 0.209 μg/ml, 2.3 μg/ml, 25.3 μg/ml and 139.5 μg/ml.

Fifty microliter aliquots of the cell suspension prepared in the above were mixed with 50μl of either solution with different monoclonal antibody concentrations, agitated at 4°C for 2 hours, added with 50μl of RPMI-1640 medium supplemented with 0.1 v/v % bovine serum albumin and also containing 4ng ^{125}I -labelled human IL-18 prepared in usual manner, and agitated at the same temperature for an additional 30 minutes. Subsequently, each cell suspension was added with 200μl mixture solution (volume ratio 1:1) of dibutylphthalate and dioctylphthalate and centrifuged at 10,000rpm and 20°C for 5 minutes, followed by collecting the resultant precipitates containing the cells which were then determined for radioactivity using "MODEL ARC-300", a gamma-ray counter commercialized by Aloka Co., Ltd, Tokyo, Japan.

In parallel, there were provided additional two sections where the monoclonal antibody was neglected, while 4ng ^{125}I -labelled human IL-18 was treated similarly as in the sample testing section with or without 4 micrograms of non-labelled human IL-18 (hereinafter referred to as "non-specific binding section" and "whole binding section" respectively). The levels of radioactivity found in "non-specific binding section" and "whole binding section" were put in Formula 1 together with that found in the sample testing section to calculate percent inhibition. The results were as shown in FIG. 1.

$$\text{Percent Inhibition} = \frac{(\text{Whole binding}) - (\text{Testing})}{(\text{Whole binding}) - (\text{Non-specific binding})} \times 100$$

Formula 1

5 Fifty microliter aliquots of an IL-18R in aqueous solution obtained by the method in Example 1-1 were added with 50μl solution with different concentrations for monoclonal antibody MAb #117-10C prepared similarly as above, agitated at 4°C for 2 hours, added with 4ng ¹²⁵I-labelled human IL-18, and agitated at 4°C for an additional 30 minutes. Subsequently, each mixture was added with 50μl of 4 mg/ml γ-globulin, allowed to stand under ice-chilling conditions for 30 minutes, added with 250μl of PBS with 20 w/v % polyethylene glycol, allowed to stand under ice-chilling conditions for an additional 30 minutes, and centrifuged at 6,000rpm at 4°C for 5 minutes, followed by collecting the resultant precipitates which were then determined for radioactivity similarly as above.

At the same time, there were provided additional two sections where the monoclonal antibody was neglected, while 4ng of ¹²⁵I-labelled human IL-18 were treated similarly as in the sample testing section with or without 4μg of non-labelled human IL-18 (hereinafter referred to as "whole binding section" and "non-specific binding section" respectively). The levels of radioactivity found in these two section were put in Formula 1 together in that found in the sample testing section to calculate percent inhibition. The results were as shown in FIG. 1.

As seen in FIG. 1, in both cases of using L428 cell and IL-18R in solution, the binding of IL-18 to L428 cell and IL-18R were inhibited much more as the concentration of monoclonal antibody MAb #117-10C elevated. This indicated that the monoclonal antibody MAb #117-10C was bound to the possible IL-18R on the surface of L428 cell in a fashion competing with IL-18, as well as that the aqueous solution obtained by the method in Example 1 did contain a protein capable of recognizing IL-18 or IL-18R and the monoclonal antibody MAb #117-10C specifically reacted with the IL-18R.

Example 1-3

Western blotting

A portion of the IL-18R in aqueous solution obtained by the method in Example 1 was sampled, added with 2/3 volume of a mixture solution of 2.5 w/v % sodium dodecyl sulfate and 50 v/v % glycerol, incubated at 37°C for 1 hour, and separated into respective proteinaceous components on conventional SDS-PAGE using 10-20% gradient gel but using no reducing agent. The proteinaceous components on the gel were transferred in usual manner to a nitrocellulose membrane which was then soaked for 1 hour in an appropriate amount of 50mM Tris-HCl buffer (pH7.5) with 10μg/ml of monoclonal antibody MAb #117-10C obtained by the methods described in Japanese Patent Application No.356,426/96 by the same applicant, 10 v/v % "BLOCK ACE", an immobilizing agent commercialized by Dainippon Seiyaku Co., Ltd., Osaka, Japan, and 0.05 v/v % "TWEEN 20", a detergent commercialized by City Chemical Corp., New York, U.S.A., and washed in 50mM Tris-HCl buffer (pH7.5) with 0.05 v/v % Tween 20 to remove the remaining antibody. The membrane was then soaked in Tris-HCl buffer (pH 7.5) with an appropriate amount of an anti-mouse immunoglobulin antibody of rabbit origin prelabelled with horse radish peroxidase, 10 v/v % "BLOCK ACE" and 0.05 v/v % "TWEEN 20" for 1 hour to effect reaction, washed in 50mM Tris-HCl buffer (pH 7.5) with 0.05 v/v % "TWEEN 20" and developed using "ECL kit", a kit for development commercialized by Amersham Corp., Arlington Heights, U.S.A.

At the same time, there was provided another section without the monoclonal antibody MAb #117-10C as control and it was treated similarly as above. The molecular weight markers were bovine serum albumin (67,000 daltons), ovalbumin (45,000 daltons), carbonic anhydrase (30,000 daltons), trypsin inhibitor (20,100 daltons) and α-lactalbumin (14,000 daltons). The results were as shown in FIG. 2.

In the gel electrophoresis in FIG. 2, Lane 2 (with monoclonal antibody) bore a distinct band of IL-18R which was never found in Lane 3 (without monoclonal antibody).

Example 1-4

Inhibition of IL-18 activity

KG-1 cells (ATCC CCL246), an established cell line derived from a patient with acute myelogenous leukemia, were suspended in RPMI-1640 medium (pH 7.2), supplemented with 10 v/v % fetal bovine serum and also containing 100μg/ml kanamycin and 18.8mM Na₂HPO₄, to give a cell density of 1×10⁷ cells/ml, added with monoclonal antibody MAb #117-10C, obtained by the method described in Japanese Patent Application No.356,426/96 by the same applicant, to give a concentration of 10μg/ml and incubated at 37°C for 30 minutes.

The KG-1 cells in suspension were distributed on 96-well microplate to give respective amounts of 50μl/well, added with 50μl of human IL-18 which had been dissolved in a fresh preparation of the same medium to give respective con-

centrations of 0ng/ml, 1.56ng/ml, 3.12ng/ml, 6.25ng/ml, 12.5ng/ml and 25ng/ml, further added with 50 μ l/well of 5 μ g/ml lipopolysaccharide in a fresh preparation of the above medium, and incubated at 37°C for 24 hours, after which each supernatant was collected and determined for IFN- γ content by conventional enzyme immunoassay. In parallel, there were provided additional sections without the monoclonal antibody MAb #117-10C for respective IL-18 concentrations as control and they were treated similarly as above. The results were as shown in FIG. 3. The IFN- γ contents in FIG. 3 were calibrated with reference to the standardized IFN- γ preparation Gg23-901-530 available from the International Institute of Health, USA, and expressed in the International Unit(IU).

The results in FIG. 3 indicated that the presence of monoclonal antibody MAb #117-10C inhibited the induction of IFN- γ by IL-18 in KG-1 cell as immunocompetent cell. This also indicated that monoclonal antibody MAb #117-10C blocked the IL-18R on the surface of KG-1 cell in a fashion competing with IL-18, thus preventing the signal transduction of IL-18 to KG-1 cell.

Example 1-5

Purification of IL-18R

Seventy-eight milligrams of a monoclonal antibody MAb #117-10C, obtained by the method described in Japanese Patent Application No.356,426/96 by the same applicant, was dissolved in an appropriate amount of distilled water and the solution was dialyzed against borate buffer (pH 8.5) with 0.5M NaCl at 4°C for 16 hours. Thereafter, in usual manner, an appropriate amount of "CNBr-ACTIVATED SEPHAROSE 4B", a CNBr-activated gel, commercialized by Pharmacia LKB Biotechnology AB, Uppsala, Sweden, was added to the dialyzed solution and allowed to react at 4°C for 18 hours under gentle stirring conditions to immobilize the monoclonal antibody MAb #117-10C on the gel.

The gel was packed into column in a plastic cylinder, equilibrated with 2mM CHAPS, charged with an IL-18R in aqueous solution obtained by the method in Example 1-1, and applied with PBS with 12mM CHAPS to remove non-adsorbed components. The column was then applied with 35mM ethylamine containing 2mM CHAPS (pH 10.8) while collecting the eluate in every 8ml fractions which were then checked for presence of IL-18R by the method in Example 1-1 using ¹²⁵I-labelled human IL-18. The chromatogram obtained in this operation was as shown in FIG.4.

As seen in FIG. 4, IL-18R was eluted in a single sharp peak when immunoaffinity chromatography using monoclonal antibody MAb #117-10C was applied to a mixture of IL-18R and contaminants such as the aqueous solution of IL-18R in Example 1-1. The fractions corresponding to this single peak were collected, pooled and lyophilized, thus obtaining a purified IL-18R in solid form.

Thereafter, a portion of the purified IL-18R was sampled, incubated in PBS at 100°C for 5 minutes, and determined for residual activity by the method in Example 1-2, resulting in no binding to IL-18 which proved that IL-18R was inactivated by heating. This would support that the nature of this receptor is proteinaceous.

Further, a portion of the purified IL-18R obtained in the above was dissolved in an appropriate amount of PBS, dialyzed against PBS at ambient temperature overnight, added with an appropriate amount of ¹²⁵I-labelled human IL-18 prepared by the method in Example 1-1 and 1mM "BS³", a polymerizing agent commercialized by Pierce, Rockford, U.S.A., and allowed to stand at 0°C for 2 hours to form a conjugate of IL-18R and ¹²⁵I-labelled human IL-18. The reaction mixture was added with Tris-HCl buffer (pH7.5), allowed to stand at 0°C for an additional 1 hour to suspend the conjugation reaction, separated into respective proteinaceous components on SDS-PAGE using a set of molecular weight markers and dithiothreitol as reducing agent, and subjected to autoradiogram analysis.

The apparent molecular weight for this conjugate of IL-18R and ¹²⁵I-labelled human IL-18 was about 50,000 to 200,000 daltons when estimated with reference to the mobility of molecular weight markers on the autoradiogram. Since the molecular weight of IL-18 is about 20,000 daltons, the molecular weight of IL-18R can be estimated about 30,000-180,000 daltons on the assumption that IL-18R binds one human IL-18 molecule.

Example 1-6

Peptide mapping of IL-18R

A purified IL-18R obtained by the method in Example 1-5 was electrophoresed on SDS-PAGE using 7.5 w/v % gel with 2 w/v % dithiothreitol as reducing agent, and the gel was then soaked for 5 minutes in a mixture solution of 40 v/v % aqueous methanol and 1 v/v % acetic acid with 0.1 w/v % Coomassie Brilliant Blue for development, and soaked for an additional 2 hours for destaining in the same solution but without Coomassie Brilliant Blue, after which the stained part in the gel, molecular weight of 80,000-110,000 daltons, was cut off, added with 50 v/v % aqueous acetonitrile containing 0.2 M (NH₄)₂CO₃ and repeatedly agitated at ambient temperature. Thereafter, the gel slices were lyophilized, added with 0.2M (NH₄)₂CO₃ (pH 8.0), allowed to stand for 5 minutes to effect swelling, added with appropriate amounts of 1mM hydrochloric acid with 0.1 μ g/ μ l "SEQUENCING GRADE MODIFIED TRYPSIN", a reagent of trypsin commer-

cialized by Promega Corp., Madison, U.S.A., and 0.2 M $(\text{NH}_4)_2\text{CO}_3$ (pH 8.9), and allowed to react at 37°C overnight. After suspending with 10 v/v % aqueous acetic acid solution, the reaction mixture was added with a mixture solution of 0.1 v/v % trifluoroacetic acid and 60 v/v % aqueous acetonitrile and agitated at ambient temperature, after which the resultant supernatant was collected, concentrated *in vacuo* and centrifugally filtered, thus obtaining a concentrate with peptide fragments.

The concentrate was charged to "μRPC C2/C18 SC2.1/10", a column for high-performance liquid chromatography commercialized by Pharmacia LKB Biotechnology AB, Uppsala, Sweden, pre-equilibrated with 0.065 v/v % trifluoroacetic acid, and then applied at a flow rate of 100μl/min with 0.055 v/v % trifluoroacetic acid containing 80 v/v % aqueous acetonitrile under linear gradient of acetonitrile increasing from 0 to 80 v/v % over 160 minutes immediately after application of the eluent. While monitoring the absorbance at a wavelength of 240nm, the eluate was fractioned to separately collect respective peptide fragments which eluted about 45, 50, 55, 58, 62, 72, 75 and 77 minutes after application of the eluent. The peptide fragments (hereinafter referred to as "peptide fragment 1", "peptide fragment 2", "peptide fragment 3", "peptide fragment 4", "peptide fragment 5", "peptide fragment 6", "peptide fragment 7" and "peptide fragment 8" in the order of elution) were analyzed in usual manner for amino acid sequence using "MODEL 473A", a protein sequencer commercialized by Perkin-Elmer Corp., Norwalk, U.S.A, revealing that the peptide fragments 1 to 8 bore the amino acid sequences of SEQ ID NOs:12 to 19 respectively. The peptide map obtained by this operation was as shown in FIG.5.

Example 2

Preparation of DNA

Example 2-1

Preparation of total RNA

In usual manner, L428 cells (FERM BP-5777) were suspended in RPMI-1640 medium (pH7.2) supplemented with 10 v/v % fetal bovine serum, and proliferated at 37°C while scaling up the cultivation. When the cell density reached a prescribed level, the proliferated cells were collected, suspended in 10mM sodium citrate (pH7.0) containing both 6M guanidine isothiocyanate and 0.5 w/v% sodium N-laurylsarcosinate, and then disrupted with a homogenizer.

Aliquots of 0.1M EDTA (pH 7.5) containing 5.7M CsCl_2 were placed in 35ml-reaction tubes, poured with the cell disruptant obtained in the above in layer over the EDTA in each tube, and subjected to ultracentrifugation at 20°C at 25,000rpm for 20 hours to collect the RNA fraction. The RNA fraction was distributed in 15ml-centrifugation tubes, added with an equivolume each of a mixture solution of chloroform/1-butanol (volume ratio 4:1), agitated for 5 minutes and centrifuged at 4°C at 10,000rpm for 10 minutes, after which the aqueous layer was collected, added with 2.5-fold volume of ethanol and allowed to stand at 20°C for 2 hours to precipitate the total RNA. The precipitate was collected, washed with 75 v/v % aqueous ethanol, and then dissolved in 0.5ml of sterilized distilled water to obtain a solution of the total RNA originating from L428 cell.

Example 2-2

Preparation of mRNA

An aqueous solution containing total RNA solution obtained by the method in Example 2-1 was added with 0.5ml of 10mM Tris-HCl buffer (pH 7.5), containing both 1mM EDTA and 0.1 w/v % sodium N-laurylsarcosinate, to bring the total volume to 1 ml. The mixture solution was added with 1 ml of "OLIGOTEX™-dT30 (SUPER)", a latex with an oligonucleotide of $(\text{dT})_{30}$ commercialized by Japan Roche K. K., Tokyo, Japan, reacted at 65°C for 5 minutes and rapidly cooled in an ice-chilling bath. Thereafter, the reaction mixture was added with 0.2ml of 5mM NaCl, incubated at 37°C for 10 minutes, centrifuged at 10,000rpm for 10 minutes to collect the resultant precipitate in pellet form which was then suspended in 0.5ml of sterilized distilled water and incubated at 65°C for 5 minutes to desorb the mRNA from the latex. The obtained solution was added with an appropriate amount of ethanol, and the resultant precipitate was collected and lyophilized to obtain a solid of mRNA.

Example 2-3

Preparation of DNA fragment encoding polypeptide

Four microliters of 25mM MgCl_2 , 2μl of 100mM Tris-HCl buffer (pH 8.3) containing 500mM KCl, 1μl of 25mM dNTP

mix, 0.5 μ l of 40units/ μ l ribonuclease inhibitor and 1 μ l of 200units/ μ l reverse transcriptase were placed in a 0.5ml-reaction tube, added with 10 ng of an mRNA, obtained by the method in Example 2-2, along with an appropriate amount of random hexanucleotides, and added with sterilized distilled water to bring the total volume of 20 μ l. The obtained mixture was incubated first at 42°C for 20 minutes, then at 99°C for 5 minutes to suspend the reaction, thus obtaining a reaction mixture containing a first strand cDNA.

Twenty microliters of the reaction mixture was added with 1 μ l of 2.5 units/ μ l "CLONED Pfu POLYMERASE", a DNA polymerase commercialized by Stratagene Cloning Systems, California, U.S.A., 10 μ l of the reaction buffer and 1 μ l of 25mM dNTP mix, both commercialized by Stratagene Cloning Systems, added with 0.1 μ g each of oligonucleotides as sense and antisense primers having respective nucleotide sequences as shown with 5'-TCAGTCGACGCCACCAT-GAATTGTAGAGAA-3' and 5'-GAAGCGGCCGCATCATTAAAGACTCGGAAAGAAC-3' which had been prepared on the basis of the amino acid sequence described in P. Parnet et al., *The Journal of Biological Chemistry*, Vol.271, pp.3967-3970 (1996), added with sterile distilled water to bring the total volume to 100 μ l. The resultant mixture was subjected first to 3-time cycles of incubating at 95°C for 1 minute, 42°C for 2 minutes and 72°C for 3 minutes in the given order, then to 35-time cycles of incubating at 95°C for 1 minute, 60°C for 2 minutes and 72°C for 3 minutes in the given order to effect PCR reaction.

Fifty nanograms of the obtained PCR product was added with 1 ng of "pCR-Script Cam SK(+)", a plasmid vector commercialized by Stratagene Cloning Systems, California, U.S.A., and then subjected to ligation reaction at 16°C for 2 hours using "DNA LIGATION KIT VERSION 2", a DNA ligation kit commercialized by Takara Syuzo, Co., Ltd., Otsu, Shiga, Japan, to insert the DNA fragment of the PCR product in the plasmid vector. A portion of the reaction product was sampled and used in usual manner to transform "XL1-BLUE MRF' KAN", an *Escherichia coli* strain commercialized by Stratagene Cloning Systems, California, U.S.A.

Example 3

Preparation of recombinant DNA

A transformant obtained by the method in Example 2-3 was inoculated in LB medium containing 30 μ g/ml chloramphenicol and cultivated at 37°C for 18 hours, after which the cells were collected from the culture and treated in usual manner to obtain the plasmid DNA. After confirming by the dideoxy method that the plasmid DNA contained the nucleotide sequence of SEQ ID NO:7, the plasmid DNA was exposed to both restriction enzymes *NotI* and *Sall*, and 100 ng of the obtained DNA fragment was added with 10ng of "pcDNAI/Amp", a plasmid vector with a modified multiple cloning site, commercialized by Invitrogen Corporation, San Diego, U.S.A., which had been predigested with both restriction enzymes *NotI* and *XhoI*, and subjected to ligation reaction at 16°C for 2 hours using "LIGATION KIT VERSION 2", a ligation kit commercialized by Takara Syuzo Co., Ltd., Otsu, Shiga, Japan. A portion of the reaction product was sampled and introduced in usual manner into "XL1-BLUE MRF' KAN", a strain of *Escherichia coli* commercialized by Stratagene Cloning Systems, California, U.S.A., to obtain a transformant "cDNA/HuIL-18R" which contained a recombinant DNA "pcDNA/HuIL-18R" of this invention. The recombinant DNA "pcDNA/HuIL-18R" was analyzed in usual manner, revealing that in the recombinant DNA, a DNA "IL-18R cDNA", which contained the nucleotide sequence of SEQ ID NO:1 encoding the polypeptide of this invention, was linked downstream the cytomegalo virus promotor *Pcmv*, as shown in FIG. 6.

Example 4

Preparation of transformant

A transformant "cDNA/HuIL-18R" obtained by the method in Example 3 was inoculated in LB medium (pH 7.5) containing 100 μ g/ml ampicillin and cultured at 37°C for 18 hours, after which the cells were collected from the culture and treated in usual manner to obtain the plasmid DNA. Separately, COS-1 cell (ATCC CRL-1650), a fibroblastic cell line derived from a kidney of African green monkey was proliferated in usual manner, and 20 micrograms of the plasmid DNA obtained in the above was introduced by conventional electroporation method into 1×10^7 COS-1 cells to obtain transformant cells which contained the DNA of this invention.

Example 5

Preparation of polypeptide

DMEM medium (pH 7.2) supplemented with 10 v/v % fetal bovine serum was distributed in flat-bottomed culture bottles, inoculated with transformant cells, obtained by the method in Example 4, to give a cell density of 1×10^5

cells/ml, and cultured at 37°C in 5 v/v % CO₂ incubator for 3 days. After removing the supernatant from the culture, PBS containing both 5mM EDTA and 0.02 w/v % NaN₃ was placed in the culture bottles to desorb the proliferated cells.

After washing in PBS, the proliferated cells were rinsed in a buffer containing 20mM HEPES, 10mM KCl, 1.5mM MgCl₂ and 0.1mM EDTA (hereinafter referred to as "hypotonic buffer"), and suspended in a fresh preparation of the hypotonic buffer to give a cell density of 2×10^7 cells/ml. The cell suspension was homogenized with a Dounce-type homogenizer under ice-chilling conditions, and the resultant homogenate was centrifuged at 15,000rpm at 5 minutes to remove both cell nuclei and intact cells, and dialyzed overnight against PBS containing 2mM CHAPS.

The dialyzed product was charged to a column of immobilized monoclonal antibody MAb #117-10C, prepared by the method in Example 1-5, which was then applied with PBS containing 12mM CHAPS to remove non-adsorbed components. Thereafter, the column was applied with 35 mM ethylamine (pH10.8) containing 2 mM CHAPS while collecting and fractionating the eluate. was applied to the column, and the eluate was fractionally collected. Each fraction was then checked for presence of the polypeptide of human origin by the method in Example 1-1 using ¹²⁵I-labelled human IL-18, selected and pooled to obtain per 10⁸ starting cells about 2 ml of an aqueous solution which contained a polypeptide with the amino acid sequence of SEQ ID NO:20. The protein content in the solution was about 10μg/ml.

The polypeptide thus obtained was studied for physicochemical properties by the methods in Example 1. As the result, the polypeptide obtained in this Example contained each amino acid sequence in SEQ ID NOs:12 to 19 as partial amino acid sequences, as well as exhibiting physiological activities which were similar to those of the IL-18R from L428 cell.

Example 6

Soluble polypeptide from human origin

Example 6-1

Preparation of recombinant DNA

One nanogram of a recombinant DNA "pcDNA/HuIL-18R" obtained by the method in Example 3, 10μl of 10xPCR buffer and 1μl of 25mM dNTP mix were placed in 0.5ml-reaction tube, added with 1 microliter of 2. units/microliter Pfu DNA polymerase, added with appropriate amounts of oligonucleotides as sense and antisense primers having respective nucleotide sequences as shown with 5'-TCAGTCGACGCCACCATGAATTGTAGAGAATTA-3' and 5'-GAAGCG-GCCGCATCATTATCTTGTGAAGACGTG-3', and with sterile distilled water to bring the total volume to 100μl. The resultant mixture was subjected first to 3-time cycles of incubating at 94°C for 1 minute, 42°C for 2 minutes and 72°C for 3 minutes in the given order, then to 35-time cycles of incubating at 94°C for 1 minute, 60°C for 2 minutes and 72°C for 3 minutes in the given order to effect PCR reaction.

Fifty nanograms of the obtained PCR product was added with 1ng of "pCR-SCRIPT SK(+)", a plasmid vector commercialized by Takara Syuzo Co. Ltd., Otsu, Shiga, Japan, and reacted using "DNA LIGATION KIT VERSION 2", a DNA ligation kit commercialized by Takara Shuzo Co. Ltd., Otsu, Shiga, Japan, at 16°C for 2 hours to insert the DNA fragment as the PCR product into the plasmid vector. A portion of the reaction product was sampled and "XL1-BLUE MRF' KAN", a strain of *Escherichia coli* commercialized by Stratagene Cloning Systems, California, U.S.A., was transformed therewith in usual manner.

The transformant obtained in the above was inoculated in LB medium (pH 7.5) containing 100μg/ml ampicillin and cultivated at 37°C for 18 hours, after which the cells were collected from the culture and treated in usual manner to obtain the plasmid DNA. After confirming by the dideoxy method that the plasmid DNA contained the nucleotide sequence of SEQ ID NO:10, the plasmid DNA was exposed to both restriction enzymes *NotI* and *SaII*, and 100 ng of the resultant DNA fragment was added with 10ng of "pEF-BOS", a plasmid vector prepared in accordance with the method described in S. Mizushima, *Nucleic Acid Research*, Vol.18, No.17, pp.5,332 (1990) with slight modification and also predigested with both restriction enzymes *NotI* and *XhoI*, and subjected to ligation reaction using "LIGATION KIT VERSION 2", a DNA ligation kit commercialized by Takara Shuzo Co., Ltd., Otsu, Shiga, Japan, at 16°C for 2 hours. A portion of the reaction product was sampled and introduced in usual manner into "XL1-BLUE MRF' KAN", a strain of *Escherichia coli* commercialized by Stratagene Cloning Systems, California, U.S.A., thus obtaining a transformant "EFHIL18R-14" which contained a recombinant DNA "pEFHIL18R-14" of this invention. The recombinant DNA "pEFHIL18R-14" was analyzed in usual manner, revealing that in the recombinant DNA, a cDNA "EFHIL18R-14 cDNA", which contained the nucleotide sequence of SEQ ID NO:6 encoding the polypeptide of this invention, was located downstream the elongation factor 1 promotor EF1αP as shown in FIG. 7.

Example 6-2

Preparation of transformant

5 A transformant "EFHIL18R-14" obtained by the method in Example 6-1 was inoculated in LB medium (pH 7.5) containing 100μg/ml ampicillin and cultivated at 37°C for 18 hours, after which the cells were collected from the culture and treated in usual manner to obtain the plasmid DNA. Separately, COS-1 cell (ATCC CRL-1650), a fibroblastoid cell line derived from a kidney of African green monkey, was proliferated in usual manner, and 20 micrograms of the plasmid DNA obtained in the above was introduced by conventional electroporation method into 1×10^7 COS-1 cells to obtain
10 transformant cells which contained the DNA of this invention.

Example 6-3

Preparation of soluble polypeptide

20 "ASF104", a serum-free nutrient culture medium commercialized by Ajinomoto Co., Inc., Tokyo, Japan, was distributed in flat-bottomed culture bottles, inoculated with transformant cells, obtained by the method in Example 6-2, to give a cell density of 1×10^5 cells/ml, and cultured in usual manner at 37°C in 5 v/v % CO₂ incubator for 3 days. The supernatant was collected from the culture and charged to a column of an immobilized monoclonal antibody #117-10C prepared by the method in Example 1-5, after which the column was applied first with PBS containing 12mM CHAPS to remove non-adsorbed components, then with 35mM ethylamine (pH 10.8) containing 2 mM CHAPS while collecting and fractionating the eluate. Each fraction was checked for presence of human soluble polypeptide by the method in Example 1-1 using ¹²⁵I-labelled human IL-18, selected and pooled to obtain per 10⁸ starting cells about 2 ml of an aqueous solution which contained a polypeptide with the amino acid sequence of SEQ ID NO:22. The protein content
25 in the solution was about 10μg/ml.

The soluble polypeptide thus obtained was studied for physicochemical properties by the method in Example 1. As the result, the soluble polypeptide obtained in this Example contained each amino acid sequences in SEQ ID NOs:12 to 17 and 19 as partial sequences, as well as exhibiting physiological activities which were similar to the IL-18R from L428 cell.

Example 7

Soluble polypeptide of human origin

One nanogram of a recombinant DNA "pEFHIL18R-14" obtained by the method in Example 6-1, 10μl of 10xPCR buffer and 1μl of 25mM dNTP mix were placed in 0.5ml-reaction tube, added with 1μl of 2.5units/μl Pfu DNA polymerase, further added with appropriate amounts of oligonucleotides as sense and antisense primers having respective nucleotide sequences as shown with 5'-TCAGTCGACGCCACCATGAATTGTAGAG-3' and 5'-GAAGCGGCCGCTCATTAGTGATGGTGATGGTGATGTGCAACATGGTTAAGCTT-3', and filled up to 100μl with sterile distilled water. The resultant mixture was subjected first to 3-time cycles of incubating at 94°C for 1 minute, 42°C for 2 minutes and 72°C for 1 minute in the given order, then to 35-time cycles of incubating at 94°C for 1 minute, 64°C for 1 minute and 72°C for 1 minute in the given order to effect PCR reaction, thus obtaining a DNA fragment which consisted of the nucleotide sequence of SEQ ID NO:5, a digestion site for restriction enzyme *Sa*I and a Kozak's sequence both linked to the 5'-terminal of the nucleotide sequence of SEQ ID NO:5, and a digestion site for restriction enzyme *Not*I and a nucleotide sequence encoding (His)₆ tag both linked to the 3'-terminal of the nucleotide sequence of SEQ ID NO:5. This DNA fragment was introduced similarly as in Example 6-1 in "XL1-Blue MRF Kan", a strain of *Escherichia coli* commercialized by Stratagene Cloning Systems, California, U.S.A., to obtain a transformant which contained a recombinant DNA "pEFHIL18RD1-2-H" according to this invention. Analysis of the recombinant DNA in usual manner confirmed that in this recombinant DNA a cDNA "HIL18RD1-2-H", which contained the nucleotide sequence of SEQ ID NO:5 encoding the polypeptide of this invention, was located downstream the elongation factor promoter EF1αP as shown in FIG. 8.

The recombinant DNA "pEFHIL18RD1-2-H" was introduced in COS-1 cells similarly as in Example 6-2 using the transformant thus obtained, and the COS-1 cells were then cultivated similarly as in Example 6-3. The supernatant of the resultant culture was concentrated with membrane filtration, and charged on a column of "Ni-NTA Spin Kit", a gel product for affinity chromatography commercialized by QIAGEN GmbH, Hilden, Germany, which was then applied with PBS containing 20mM imidazole to remove the non-adsorbed fractions. Thereafter, the column was applied with PBS containing 250mM imidazole, and the eluate was collected in fractions while checking the presence of human soluble polypeptide in each fraction by the method in Example 1-1 using ¹²⁵I-labelled human IL-18, after which the fractions

with the polypeptide were collected and pooled, thus obtaining about 2ml of an aqueous solution containing the polypeptide with the amino acid sequence of SEQ ID NO:23 per starting 10^8 cells. The protein content in the solution was about 10µg/ml.

The soluble polypeptide thus obtained was studied for physicochemical properties by the method in Example 1. As the result, the soluble polypeptide obtained in this Example contained a part or whole of each amino acid sequences in SEQ ID NOs:14 to 16 and 19 as partial amino acid sequences, as well as exhibiting physiological activities which were similar to those of IL-18R from L428 cell.

Example 8

Soluble polypeptide of human origin

A transformant containing a recombinant DNA "pEFHIL18RD1-H" according to this invention was prepared similarly as in Example 7, except that sense and antisense primers were replaced with oligonucleotides having respective nucleotide sequences as shown with 5'-TCAGTCGACGCCACCATGAATTGTAGAG-3' and GAAGCGGCCGCT-CATTAGTGATGGTGATGGTGATGTCTTTCAGTGAAACAGCT-3'. Analysis of the recombinant DNA in usual manner confirmed that in the recombinant DNA a cDNA "HIL18RD1-H", which contained the nucleotide sequence of SEQ ID NO:3 encoding the polypeptide of this invention, was located downstream the elongation factor promotor EF1αP as shown in FIG. 9. Thereafter, similarly as in Example 7, the recombinant DNA was introduced in COS-1 cells and brought into expression, thus obtaining about 2ml of an aqueous solution containing a polypeptide with the amino acid sequence of SEQ ID NO:24 per 10^8 starting cells. The protein content in the solution was about 10µg/ml.

The polypeptide of this invention thus obtained were studied for physicochemical properties by the method in Example 1. As the result, the soluble polypeptide obtained in this Example contained each amino acid sequences of SEQ ID NOs:14 and 15 as partial amino acid sequences, as well as exhibiting physiological activities which were similar to those of the IL-18R from L428 cell.

Example 9

Soluble polypeptide of mouse origin

Example 9-1

Preparation of recombinant DNA

A reaction product containing a first strand cDNA was obtained by subjecting an mRNA, prepared in usual manner from mouse liver, in place with that from L428 cell to the same reaction to synthesize first strand cDNA as in Example 2-3. The reaction product was treated by the same PCR method as in Example 2-3, except that the sense and antisense primers were replaced with oligonucleotides having respective nucleotide sequence as shown with 5'-TCAGTCGACGCCACCATGCATCATGAAGAA-3' and 5'-GAAGCGGCCGCGCATCATTAGTGATGGTGATGGTGATGTGTAAGACATGGCC-3', which had been prepared on the basis of the amino acid sequence described in P. Parinet et al., *The Journal of Biological Chemistry*, Vol.271, pp.3,967-3,970 (1996) and also the nucleotide sequence of SEQ ID NO:1. This operation gave a DNA fragment which comprised the nucleotide sequence of SEQ ID NO:11, a digestion site for restriction enzyme *Sall* linked to the 5'-terminal in the nucleotide sequence of the SEQ ID NO:11, and a cleavage site for restriction enzyme *NotI* and a nucleotide sequence encoding (His)₆ tag both linked to the 3'-terminal in the nucleotide sequence of the SEQ ID NO:11.

According to the method in Example 6-1, this DNA fragment was introduced into "XL1-BLUE MRF' KAN", a strain of *Escherichia coli* commercialized by Stratagene Cloning Systems, California, U.S.A., to transform. After a plasmid DNA was collected from the transformant and confirmed to contain the nucleotide sequence of SEQ ID NO:11, the plasmid DNA was introduced into "XL1-BLUE MRF' KAN", a strain of *Escherichia coli* strain commercialized by Stratagene Cloning Systems, California, U.S.A., to obtain a transformant "EFMIL18RSHT" which contains a recombinant DNA "pEFMIL18RSHT" according to this invention. Analysis in usual manner confirmed that in the recombinant DNA "pEFMIL18RSHT" a cDNA "EFMIL18RSHT cDNA", which contained the nucleotide sequence of SEQ ID NO:4 encoding the polypeptide of this invention, was linked to downstream of the elongation factor 1 promotor EF1αP, as shown in FIG. 8.

Example 9-2Preparation of transformant and soluble polypeptide

5 According to the method in Example 6-2, a plasmid DNA was collected from a transformant "EFMIL18RSHT" obtained by the method in Example 9-1, and introduced into COS-1 cells to obtain transformant cells which contained a DNA encoding a soluble polypeptide of mouse origin.

10 "ASF104", a serum-free nutrient culture medium commercialized by Ajinomoto Co., Inc., Tokyo, Japan, was distributed in flat-bottomed culture bottles, inoculated with the transformed COS-1 cells to give a cell density of 1×10^5 cells/ml, and cultivated in usual manner at 37°C in 5 v/v % CO₂ incubator for 3 days. The supernatant was collected from the resultant culture and charged to a column of "Ni-NTA", a gel product for affinity chromatography, commercialized by QIAGEN GmbH, Hilden, Germany, after which the column was applied first with PBS containing 20mM imidazole to remove non-adsorbed components, then with PBS containing 250mM imidazole while collecting and fractionating the eluate. The fractions were checked for presence of mouse soluble polypeptide by the method in Example 1-1 using ¹²⁵I-labelled mouse IL-18, selected and pooled, thus obtaining per 10⁸ starting cells about 2 ml of an aqueous solution which contained a polypeptide with the amino acid sequence of SEQ ID NO:25. The protein content in the solution was about 100µg/ml. The soluble polypeptide thus obtained was studied in accordance with the method in Example 1, revealing that it efficiently neutralized mouse IL-18.

Example 10Liquid agent

25 Either polypeptide obtained by the method in Examples 5 to 8 was separately dissolved in aliquots of physiological saline containing as stabilizer 1 w/v % "TREHAOSE", a powdered crystalline trehalose commercialized by Hayashibara Co., Ltd., Okayama, Japan, to give respective concentration of 1 mg/ml, and the resultant mixtures were separately and sterilely filtered with membrane in usual manner to obtain four distinct liquid agents.

The products, which are excellent in stability, are useful as injection, ophthalmic solution and collunarium in treatment and prevention of susceptible diseases including autoimmune diseases.

Example 11Dried injection

35 One hundred milligrams of either polypeptide obtained by the methods in Example 5 to 8 was separately dissolved in aliquots of physiological saline containing 1 w/v % sucrose as stabilizer, the resultant solutions were separately and sterilely filtered with membrane, distributed in vials in every 1 ml aliquot, lyophilized and sealed in usual manner to obtain four distinct pulverized agents.

40 The products, which are excellent in stability, are useful as dried injection in treatment and prevention of susceptible diseases including autoimmune diseases.

Example 12Ointment

45 "HI-BIS-WAKO 104", a carboxyvinylpolymer commercialized by Wako Pure Chemicals, Tokyo, Japan, and "TREHAOSE", a powdered crystalline trehalose commercialized by Hayashibara Co., Ltd., Okayama, Japan, were dissolved in sterilized distilled water to give respective concentrations of 1.4 w/w % and 2.0 w/w %, and either polypeptide obtained by the methods in Examples 5 to 8 was separately mixed with aliquots of the resultant solution to homogeneity, and adjusted to pH7.2 to obtain four distinct paste agents containing about 1 mg/g of the polypeptide of this invention each.

55 The products, which are excellent in both spreadability and stability, are useful as ointment in treatment and prevention of susceptible diseases including autoimmune diseases.

Example 13Tablet

5 Aliquots of "FINETOSE", a pulverized anhydrous crystalline alpha-maltose commercialized by Hayashibara Co., Ltd., Okayama, Japan, were separately admixed with either polypeptide, obtained by the methods in Examples 5 to 8, and aliquots of "LUMIN" as cell activator, [bis-4-(1-ethylquinoline)][γ -4'-(1-ethylquinoline)] pentamethionine cyanine, to homogeneity, and the resultant mixtures were separately tableted in usual manner to obtain four distinct types of tablets, about 200 mg each, containing about 1mg/tablet of the polypeptide of this invention and also 1mg/tablet of LUMIN each.

10 The products, which are excellent in swallowability and stability and also bears an cell activating property, are useful as tablet in treatment and prevention of susceptible diseases including autoimmune diseases.

ExperimentAcute toxicity test

15 In usual manner, a variety of agents, obtained by the methods in Examples 8 to 11, were percutaneously or orally administrated or intraperitoneally injected to 8 week-old mice. As the result, the LD₅₀ of each sample was proved about 20 1 mg or higher per body weight of mouse in terms of the amount of the polypeptide, regardless of administration route. This does support that the polypeptide of this invention is safe when incorporated in pharmaceuticals directed to use in mammals including human.

25 As explained above, this invention is based on the discovery of a novel receptor protein which recognizes IL-18. The polypeptide of this invention exhibits a remarkable efficacy in relief of rejection reaction associated with grafts of organs and also in treatment and prevention of various disease resulting from excessive immunoreaction because the polypeptide bears properties of suppressing and regulating immunoreaction in mammals including human. Further, the polypeptide of this invention is useful in clarification of physiological activities of IL-18, establishment of hybridoma cells which are capable of producing monoclonal antibodies specific to IL-18R, and also affinity chromatography and labelled assay to purify and detect IL-18. In addition, the polypeptide of this invention, in particular, that in soluble form is useful 30 in screening *in vivo* and *in vitro* agonists and antagonists to IL-18. The polypeptide of this invention, which bears these outstanding usefulness, can be easily prepared in desired amounts by the process according to this invention using recombinant DNA techniques.

35 This invention, which exhibits these remarkable effects, would be very significant and contributive to the art.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

NAME:KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
KENKYUJO

(ii) TITLE OF INVENTION:POLYPEPTIDES

(iii) NUMBER OF SEQUENCES:27

(iv) ADDRESS:

(A) ADDRESSEE:KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU
KAGAKU KENKYUJO

(B) STREET:2-3, 1-CHOME, SHIMOISHII

(C) CITY:OKAYAMA

(E) COUNTRY:JAPAN

(F) POSTAL CODE (ZIP):700

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE:Floppy disk

(B) COMPUTER:IBM PC compatible

(C) OPERATING SYSTEM:PC-DOS/MS-DOS

(vii) PRIOR APPLICATION DATA:

(A1) APPLICATION NUMBER: JP 74,697/97

(B1) FILING DATE:March 12, 1997

(vii) PRIOR APPLICATION DATA:

(A2) APPLICATION NUMBER: JP 215,488/97

(B2) FILING DATE:July 28, 1997

(vii) PRIOR APPLICATION DATA:

(A3) APPLICATION NUMBER: JP 291,837/97

(B3) FILING DATE:October 9, 1997

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:1563 base pairs

(B) TYPE:nucleic acid

(C) strandedness:double

(D) TOPOLOGY:linear

(ii) MOLECULE TYPE:cDNA

(ix) FEATURE:

(A) NAME/KEY:mat peptide

(B) LOCATION:1..1563

(C) IDENTIFICATION METHOD:E

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:1:

GAA TCT TGT ACT TCA CGT CCC CAC ATT ACT GTG GTT GAA GGG GAA CCT
48
Glu Ser Cys Thr Ser Arg Pro His Ile Thr Val Val Glu Gly Glu Pro
1 5 10 15
TTC TAT CTG AAA CAT TGC TCG TGT TCA CTT GCA CAT GAG ATT GAA ACA
96
Phe Tyr Leu Lys His Cys Ser Cys Ser Leu Ala His Glu Ile Glu Thr
20 25 30
ACC ACC AAA AGC TGG TAC AAA AGC AGT GGA TCA CAG GAA CAT GTG GAG
144
Thr Thr Lys Ser Trp Tyr Lys Ser Ser Gly Ser Gln Glu His Val Glu

EP 0 864 585 A1

		35		40		45											
	CTG	AAC	CCA	AGG	AGT	TCC	TCG	AGA	ATT	GCT	TTG	CAT	GAT	TGT	GTT	TTG	
5	192	Leu	Asn	Pro	Arg	Ser	Ser	Ser	Arg	Ile	Ala	Leu	His	Asp	Cys	Val	Leu
		50					55					60					
	GAG	TTT	TGG	CCA	GTT	GAG	TTG	AAT	GAC	ACA	GGA	TCT	TAC	TTT	TTC	CAA	
	240	Glu	Phe	Trp	Pro	Val	Glu	Leu	Asn	Asp	Thr	Gly	Ser	Tyr	Phe	Phe	Gln
10	65	ATG	AAA	AAT	TAT	ACT	CAG	AAA	TGG	AAA	TTA	AAT	GTC	ATC	AGA	AGA	80
	288	Met	Lys	Asn	Tyr	Thr	Gln	Lys	Trp	Lys	Leu	Asn	Val	Ile	Arg	Arg	Asn
					85						90				95		
	AAA	CAC	AGC	TGT	TTC	ACT	GAA	AGA	CAA	GTA	ACT	AGT	AAA	ATT	GTG	GAA	
	336	Lys	His	Ser	Cys	Phe	Thr	Glu	Arg	Gln	Val	Thr	Ser	Lys	Ile	Val	Glu
15				100					105					110			
	GTT	AAA	AAA	TTT	TTT	CAG	ATA	ACC	TGT	GAA	AAC	AGT	TAC	TAT	CAA	ACA	
	384	Val	Lys	Lys	Phe	Phe	Gln	Ile	Thr	Cys	Glu	Asn	Ser	Tyr	Tyr	Gln	Thr
20			115				120					125					
	CTG	GTC	AAC	AGC	ACA	TCA	TTG	TAT	AAG	AAC	TGT	AAA	AAG	CTA	CTA	CTG	
	432	Leu	Val	Asn	Ser	Thr	Ser	Leu	Tyr	Lys	Asn	Cys	Lys	Lys	Leu	Leu	Leu
		130					135				140						
	GAG	AAC	AAT	AAA	AAC	CCA	ACG	ATA	AAG	AAG	AAC	GCC	GAG	TTT	GAA	GAT	
	480	Glu	Asn	Asn	Lys	Asn	Pro	Thr	Ile	Lys	Lys	Asn	Ala	Glu	Phe	Glu	Asp
25	145					150					155					160	
	CAG	GGG	TAT	TAC	TCC	TGC	GTG	CAT	TTC	CTT	CAT	CAT	AAT	GGA	AAA	CTA	
	528	Gln	Gly	Tyr	Tyr	Ser	Cys	Val	His	Phe	Leu	His	His	Asn	Gly	Lys	Leu
					165				170						175		
30	576	TTT	AAT	ATC	ACC	AAA	ACC	TTC	AAT	ATA	ACA	ATA	GTG	GAA	GAT	CGC	AGT
		Phe	Asn	Ile	Thr	Lys	Thr	Phe	Asn	Ile	Thr	Ile	Val	Glu	Asp	Arg	Ser
				180				185					190				
	AAT	ATA	GTT	CCG	GTT	CTT	CTT	GGA	CCA	AAG	CTT	AAC	CAT	GTT	GCA	GTG	
	624	Asn	Ile	Val	Pro	Val	Leu	Leu	Gly	Pro	Lys	Leu	Asn	His	Val	Ala	Val
35			195				200					205					
	GAA	TTA	GGA	AAA	AAC	GTA	AGG	CTC	AAC	TGC	TCT	GCT	TTG	CTG	AAT	GAA	
	672	Glu	Leu	Gly	Lys	Asn	Val	Arg	Leu	Asn	Cys	Ser	Ala	Leu	Leu	Asn	Glu
40	210					215					220						
	GAG	GAT	GTA	ATT	TAT	TGG	ATG	TTC	GGG	GAA	GAA	AAT	GGA	TCG	GAT	CCT	
	720	Glu	Asp	Val	Ile	Tyr	Trp	Met	Phe	Gly	Glu	Glu	Asn	Gly	Ser	Asp	Pro
	225					230					235					240	
	AAT	ATA	CAT	GAA	GAG	AAA	GAA	ATG	AGA	ATT	ATG	ACT	CCA	GAA	GGC	AAA	
	768	Asn	Ile	His	Glu	Glu	Lys	Glu	Met	Arg	Ile	Met	Thr	Pro	Glu	Gly	Lys
45					245				250						255		
	TGG	CAT	GCT	TCA	AAA	GTA	TTG	AGA	ATT	GAA	AAT	ATT	GGT	GAA	AGC	AAT	
	816	Trp	His	Ala	Ser	Lys	Val	Leu	Arg	Ile	Glu	Asn	Ile	Gly	Glu	Ser	Asn
				260				265				270					
50	864	CTA	AAT	GTT	TTA	TAT	AAT	TGC	ACT	GTG	GCC	AGC	ACG	GGA	GGC	ACA	GAC
		Leu	Asn	Val	Leu	Tyr	Asn	Cys	Thr	Val	Ala	Ser	Thr	Gly	Gly	Thr	Asp
			275					280					285				

55

EP 0 864 585 A1

	ACC	AAA	AGC	TTC	ATC	TTG	GTG	AGA	AAA	GAC	ATG	GCT	GAT	ATC	CCA	GGC
	912															
	Thr	Lys	Ser	Phe	Ile	Leu	Val	Arg	Lys	Asp	Met	Ala	Asp	Ile	Pro	Gly
5		290					295					300				
	CAC	GTC	TTC	ACA	AGA	GGA	ATG	ATC	ATA	GCT	GTT	TTG	ATC	TTG	GTG	GCA
	960															
	His	Val	Phe	Thr	Arg	Gly	Met	Ile	Ile	Ala	Val	Leu	Ile	Leu	Val	Ala
	305					310					315					320
	GTA	GTG	TGC	CTA	GTG	ACT	GTG	TGT	GTC	ATT	TAT	AGA	GTT	GAC	TTG	GTT
10	1008															
	Val	Val	Cys	Leu	Val	Thr	Val	Cys	Val	Ile	Tyr	Arg	Val	Asp	Leu	Val
					325					330					335	
	CTA	TTT	TAT	AGA	CAT	TTA	ACG	AGA	AGA	GAT	GAA	ACA	TTA	ACA	GAT	GGA
	1056															
	Leu	Phe	Tyr	Arg	His	Leu	Thr	Arg	Arg	Asp	Glu	Thr	Leu	Thr	Asp	Gly
15				340					345					350		
	AAA	ACA	TAT	GAT	GCT	TTT	GTG	TCT	TAC	CTA	AAA	GAA	TGC	CGA	CCT	GAA
	1104															
	Lys	Thr	Tyr	Asp	Ala	Phe	Val	Ser	Tyr	Leu	Lys	Glu	Cys	Arg	Pro	Glu
			355					360					365			
	AAT	GGA	GAG	GAG	CAC	ACC	TTT	GCT	GTG	GAG	ATT	TTG	CCC	AGG	GTG	TTG
20	1152															
	Asn	Gly	Glu	Glu	His	Thr	Phe	Ala	Val	Glu	Ile	Leu	Pro	Arg	Val	Leu
		370					375					380				
	GAG	AAA	CAT	TTT	GGG	TAT	AAG	TTA	TGC	ATA	TTT	GAA	AGG	GAT	GTA	GTG
	1200															
	Glu	Lys	His	Phe	Gly	Tyr	Lys	Leu	Cys	Ile	Phe	Glu	Arg	Asp	Val	Val
25					390						395					400
	CCT	GGA	GGA	GCT	GTT	GTT	GAT	GAA	ATC	CAC	TCA	CTG	ATA	GAG	AAA	AGC
	1248															
	Pro	Gly	Gly	Ala	Val	Val	Asp	Glu	Ile	His	Ser	Leu	Ile	Glu	Lys	Ser
					405					410					415	
	CGA	AGA	CTA	ATC	ATT	GTC	CTA	AGT	AAA	AGT	TAT	ATG	TCT	AAT	GAG	GTC
30	1296															
	Arg	Arg	Leu	Ile	Ile	Val	Leu	Ser	Lys	Ser	Tyr	Met	Ser	Asn	Glu	Val
				420					425					430		
	AGG	TAT	GAA	CTT	GAA	AGT	GGA	CTC	CAT	GAA	GCA	TTG	GTG	GAA	AGA	AAA
	1344															
	Arg	Tyr	Glu	Leu	Glu	Ser	Gly	Leu	His	Glu	Ala	Leu	Val	Glu	Arg	Lys
35			435					440					445			
	ATT	AAA	ATA	ATC	TTA	ATT	GAA	TTT	ACA	CCT	GTT	ACT	GAC	TTC	ACA	TTC
	1392															
	Ile	Lys	Ile	Ile	Leu	Ile	Glu	Phe	Thr	Pro	Val	Thr	Asp	Phe	Thr	Phe
		450					455					460				
	TTG	CCC	CAA	TCA	CTA	AAG	CTT	TTG	AAA	TCT	CAC	AGA	GTT	CTG	AAG	TGG
40	1440															
	Leu	Pro	Gln	Ser	Leu	Lys	Leu	Leu	Lys	Ser	His	Arg	Val	Leu	Lys	Trp
						470					475					480
	AAG	GCC	GAT	AAA	TCT	CTT	TCT	TAT	AAC	TCA	AGG	TTC	TGG	AAG	AAC	CTT
	1488															
	Lys	Ala	Asp	Lys	Ser	Leu	Ser	Tyr	Asn	Ser	Arg	Phe	Trp	Lys	Asn	Leu
45					485				490						495	
	CTT	TAC	TTA	ATG	CCT	GCA	AAA	ACA	GTC	AAG	CCA	GGT	AGA	GAC	GAA	CCG
	1536															
	Leu	Tyr	Leu	Met	Pro	Ala	Lys	Thr	Val	Lys	Pro	Gly	Arg	Asp	Glu	Pro
				500					505					510		
	GAA	GTC	TTG	CCT	GTT	CTT	TCC	GAG	TCT							
50	1563															
	Glu	Val	Leu	Pro	Val	Leu	Ser	Glu	Ser							
			515					520								

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1557 base pairs

(B) TYPE: nucleic acid

(C) strandedness: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: mat peptide

(B) LOCATION: 1..1557

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCA AAA AGT TGT ATT CAC CGA TCA CAA ATT CAT GTG GTA GAG GGA GAA
 48
 Ser Lys Ser Cys Ile His Arg Ser Gln Ile His Val Val Glu Gly Glu
 1 5 10 15
 CCT TTT TAT CTG AAG CCA TGT GGC ATA TCT GCA CCA GTG CAC AGG AAT
 96
 Pro Phe Tyr Leu Lys Pro Cys Gly Ile Ser Ala Pro Val His Arg Asn
 20 25 30
 GAA ACA GCC ACC ATG AGA TGG TTC AAA GGC AGT GCT TCA CAT GAG TAT
 144
 Glu Thr Ala Thr Met Arg Trp Phe Lys Gly Ser Ala Ser His Glu Tyr
 35 40 45
 AGA GAG CTG AAC AAC AGA AGC TCG CCC AGA GTC ACT TTT CAT GAT CAC
 192
 Arg Glu Leu Asn Asn Arg Ser Ser Pro Arg Val Thr Phe His Asp His
 50 55 60
 ACC TTG GAA TTC TGG CCA GTT GAG ATG GAG GAT GAG GGA ACG TAC ATT
 240
 Thr Leu Glu Phe Trp Pro Val Glu Met Glu Asp Glu Gly Thr Tyr Ile
 65 70 75 80
 TCT CAA GTC GGA AAT GAT CGT CGC AAT TGG ACC TTA AAT GTC ACC AAA
 288
 Ser Gln Val Gly Asn Asp Arg Arg Asn Trp Thr Leu Asn Val Thr Lys
 85 90 95
 AGA AAC AAA CAC AGC TGT TTC TCT GAC AAG CTC GTG ACA AGC AGA GAT
 336
 Arg Asn Lys His Ser Cys Phe Ser Asp Lys Leu Val Thr Ser Arg Asp
 100 105 110
 GTT GAA GTT AAC AAA TCT CTG CAT ATC ACT TGT AAG AAT CCT AAC TAT
 384
 Val Glu Val Asn Lys Ser Leu His Ile Thr Cys Lys Asn Pro Asn Tyr
 115 120 125
 GAA GAG CTG ATC CAG GAC ACA TGG CTG TAT AAG AAC TGT AAG GAA ATA
 432
 Glu Glu Leu Ile Gln Asp Thr Trp Leu Tyr Lys Asn Cys Lys Glu Ile
 130 135 140
 TCC AAA ACC CCA AGG ATC CTG AAG GAT GCC GAG TTT GGA GAT GAG GGC
 480
 Ser Lys Thr Pro Arg Ile Leu Lys Asp Ala Glu Phe Gly Asp Glu Gly
 145 150 155 160
 TAC TAC TCC TGC GTG TTT TCT GTC CAC CAT AAT GGG ACA CGG TAC AAC
 528
 Tyr Tyr Ser Cys Val Phe Ser Val His His Asn Gly Thr Arg Tyr Asn
 165 170 175
 ATC ACC AAG ACT GTC AAT ATA ACA GTT ATT GAA GGA AGG AGT AAA GTA
 576
 Ile Thr Lys Thr Val Asn Ile Thr Val Ile Glu Gly Arg Ser Lys Val
 180 185 190

EP 0 864 585 A1

	ACT	CCA	GCT	ATT	TTA	GGA	CCA	AAG	TGT	GAG	AAG	GTT	GGT	GTA	GAA	CTA
	624															
5	Thr	Pro	Ala	Ile	Leu	Gly	Pro	Lys	Cys	Glu	Lys	Val	Gly	Val	Glu	Leu
			195					200					205			
	GGA	AAG	GAT	GTG	GAG	TTG	AAC	TGC	AGT	GCT	TCA	TTG	AAT	AAA	GAC	GAT
	672															
	Gly	Lys	Asp	Val	Glu	Leu	Asn	Cys	Ser	Ala	Ser	Leu	Asn	Lys	Asp	Asp
		210					215					220				
10	CTG	TTT	TAT	TGG	AGC	ATC	AGG	AAA	GAG	GAC	AGC	TCA	GAC	CCT	AAT	GTG
	720															
	Leu	Phe	Tyr	Trp	Ser	Ile	Arg	Lys	Glu	Asp	Ser	Ser	Asp	Pro	Asn	Val
	225					230					235					240
	CAA	GAA	GAC	AGG	AAG	GAG	ACG	ACA	ACA	TGG	ATT	TCT	GAA	GGC	AAA	CTG
	768															
15	Gln	Glu	Asp	Arg	Lys	Glu	Thr	Thr	Thr	Trp	Ile	Ser	Glu	Gly	Lys	Leu
					245					250					255	
	CAT	GCT	TCA	AAA	ATA	CTG	AGA	TTT	CAG	AAA	ATT	ACT	GAA	AAC	TAT	CTC
	816															
	His	Ala	Ser	Lys	Ile	Leu	Arg	Phe	Gln	Lys	Ile	Thr	Glu	Asn	Tyr	Leu
				260					265					270		
20	AAT	GTT	TTA	TAT	AAT	TGC	ACC	GTG	GCC	AAC	GAA	GAA	GCC	ATA	GAC	ACC
	864															
	Asn	Val	Leu	Tyr	Asn	Cys	Thr	Val	Ala	Asn	Glu	Glu	Ala	Ile	Asp	Thr
			275					280					285			
	AAG	AGC	TTC	GTC	TTG	GTG	AGA	AAA	GAA	ATA	CCT	GAT	ATC	CCA	GGC	CAT
	912															
25	Lys	Ser	Phe	Val	Leu	Val	Arg	Lys	Glu	Ile	Pro	Asp	Ile	Pro	Gly	His
		290					295					300				
	GTC	TTT	ACA	GGA	GGA	GTA	ACT	GTG	CTT	GTT	CTC	GCC	TCT	GTG	GCA	GCA
	960															
	Val	Phe	Thr	Gly	Gly	Val	Thr	Val	Leu	Val	Leu	Ala	Ser	Val	Ala	Ala
	305					310					315					320
30	GTG	TGT	ATA	GTG	ATT	TTG	TGT	GTC	ATT	TAT	AAA	GTT	GAC	TTG	GTT	CTG
	1008															
	Val	Cys	Ile	Val	Ile	Leu	Cys	Val	Ile	Tyr	Lys	Val	Asp	Leu	Val	Leu
					325					330					335	
	TTC	TAT	AGG	CGC	ATA	GCG	GAA	AGA	GAC	GAG	ACA	CTA	ACA	GAT	GGT	AAA
	1056															
35	Phe	Tyr	Arg	Arg	Ile	Ala	Glu	Arg	Asp	Glu	Thr	Leu	Thr	Asp	Gly	Lys
				340					345					350		
	ACA	TAT	GAT	GCC	TTT	GTG	TCT	TAC	CTG	AAA	GAG	TGT	CAT	CCT	GAG	AAT
	1104															
	Thr	Tyr	Asp	Ala	Phe	Val	Ser	Tyr	Leu	Lys	Glu	Cys	His	Pro	Glu	Asn
			355					360					365			
40	AAA	GAA	GAG	TAT	ACT	TTT	GCT	GTG	GAG	ACG	TTA	CCC	AGG	GTC	CTG	GAG
	1152															
	Lys	Glu	Glu	Tyr	Thr	Phe	Ala	Val	Glu	Thr	Leu	Pro	Arg	Val	Leu	Glu
		370					375					380				
	AAA	CAG	TTT	GGG	TAT	AAG	TTA	TGC	ATA	TTT	GAA	AGA	GAT	GTG	GTG	CCT
	1200															
45	Lys	Gln	Phe	Gly	Tyr	Lys	Leu	Cys	Ile	Phe	Glu	Arg	Asp	Val	Val	Pro
	385					390					395					400
	GGC	GGA	GCT	GTT	GTC	GAG	GAG	ATC	CAT	TCA	CTG	ATA	GAG	AAA	AGC	CGG
	1248															
	Gly	Gly	Ala	Val	Val	Glu	Glu	Ile	His	Ser	Leu	Ile	Glu	Lys	Ser	Arg
					405					410					415	
50	AGG	CTA	ATC	ATC	GTT	CTC	AGC	CAG	AGT	TAC	CTG	ACT	AAC	GGA	GCC	AGG
	1296															
	Arg	Leu	Ile	Ile	Val	Leu	Ser	Gln	Ser	Tyr	Leu	Thr	Asn	Gly	Ala	Arg
				420					425					430		
	CGT	GAG	CTC	GAG	AGT	GGA	CTC	CAC	GAA	GCA	CTG	GTA	GAG	AGG	AAG	ATT

55

1344
 Arg Glu Leu Glu Ser Gly Leu His Glu Ala Leu Val Glu Arg Lys Ile
 435 440 445
 5 AAG ATC ATC TTA ATT GAG TTT ACT CCA GCC AGC AAC ATC ACC TTT CTC
 1392
 Lys Ile Ile Leu Ile Glu Phe Thr Pro Ala Ser Asn Ile Thr Phe Leu
 450 455 460
 CCC CCG TCG CTG AAA CTC CTG AAG TCC TAC AGA GTT CTA AAA TGG AGG
 1440
 10 Pro Pro Ser Leu Lys Leu Leu Lys Ser Tyr Arg Val Leu Lys Trp Arg
 465 470 475 480
 GCT GAC AGT CCC TCC ATG AAC TCA AGG TTC TGG AAG AAT CTT GTT TAC
 1488
 Ala Asp Ser Pro Ser Met Asn Ser Arg Phe Trp Lys Asn Leu Val Tyr
 485 490 495
 15 CTG ATG CCC GCA AAA GCC GTC AAG CCA TGG AGA GAG GAG TCG GAG GCG
 1536
 Leu Met Pro Ala Lys Ala Val Lys Pro Trp Arg Glu Glu Ser Glu Ala
 500 505 510
 CGG TCT GTT CTC TCA GCA CCT
 1557
 20 Arg Ser Val Leu Ser Ala Pro
 515

(4) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) strandedness: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat peptide
 (B) LOCATION: 1..312
 (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAA TCT TGT ACT TCA CGT CCC CAC ATT ACT GTG GTT GAA GGG GAA CCT
 48
 35 Glu Ser Cys Thr Ser Arg Pro His Ile Thr Val Val Glu Gly Glu Pro
 1 5 10 15
 TTC TAT CTG AAA CAT TGC TCG TGT TCA CTT GCA CAT GAG ATT GAA ACA
 96
 Phe Tyr Leu Lys His Cys Ser Cys Ser Leu Ala His Glu Ile Glu Thr
 20 25 30
 40 ACC ACC AAA AGC TGG TAC AAA AGC AGT GGA TCA CAG GAA CAT GTG GAG
 144
 Thr Thr Lys Ser Trp Tyr Lys Ser Ser Gly Ser Gln Glu His Val Glu
 35 40 45
 CTG AAC CCA AGG AGT TCC TCG AGA ATT GCT TTG CAT GAT TGT GTT TTG
 192
 45 Leu Asn Pro Arg Ser Ser Ser Arg Ile Ala Leu His Asp Cys Val Leu
 50 55 60
 GAG TTT TGG CCA GTT GAG TTG AAT GAC ACA GGA TCT TAC TTT TTC CAA
 240
 Glu Phe Trp Pro Val Glu Leu Asn Asp Thr Gly Ser Tyr Phe Phe Gln
 65 70 75 80
 50 ATG AAA AAT TAT ACT CAG AAA TGG AAA TTA AAT GTC ATC AGA AGA AAT
 288
 Met Lys Asn Tyr Thr Gln Lys Trp Lys Leu Asn Val Ile Arg Arg Asn
 85 90 95

55

AAA CAC AGC TGT TTC ACT GAA AGA
 312
 Lys His Ser Cys Phe Thr Glu Arg
 100

(5) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 921 base pairs
 (B) TYPE: nucleic acid
 (C) strandedness: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: mat peptide
 (B) LOCATION: 1..921
 (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCA AAA AGT TGT ATT CAC CGA TCA CAA ATT CAT GTG GTA GAG GGA GAA
 48
 Ser Lys Ser Cys Ile His Arg Ser Gln Ile His Val Val Glu Gly Glu
 1 5 10 15
 CCT TTT TAT CTG AAG CCA TGT GGC ATA TCT GCA CCA GTG CAC AGG AAT
 96
 Pro Phe Tyr Leu Lys Pro Cys Gly Ile Ser Ala Pro Val His Arg Asn
 20 25 30
 GAA ACA GCC ACC ATG AGA TGG TTC AAA GGC AGT GCT TCA CAT GAG TAT
 144
 Glu Thr Ala Thr Met Arg Trp Phe Lys Gly Ser Ala Ser His Glu Tyr
 35 40 45
 AGA GAG CTG AAC AAC AGA AGC TCG CCC AGA GTC ACT TTT CAT GAT CAC
 192
 Arg Glu Leu Asn Asn Arg Ser Ser Pro Arg Val Thr Phe His Asp His
 50 55 60
 ACC TTG GAA TTC TGG CCA GTT GAG ATG GAG GAT GAG GGA ACG TAC ATT
 240
 Thr Leu Glu Phe Trp Pro Val Glu Met Glu Asp Glu Gly Thr Tyr Ile
 65 70 75 80
 TCT CAA GTC GGA AAT GAT CGT CGC AAT TGG ACC TTA AAT GTC ACC AAA
 288
 Ser Gln Val Gly Asn Asp Arg Arg Asn Trp Thr Leu Asn Val Thr Lys
 85 90 95
 AGA AAC AAA CAC AGC TGT TTC TCT GAC AAG CTC GTG ACA AGC AGA GAT
 336
 Arg Asn Lys His Ser Cys Phe Ser Asp Lys Leu Val Thr Ser Arg Asp
 100 105 110
 GTT GAA GTT AAC AAA TCT CTG CAT ATC ACT TGT AAG AAT CCT AAC TAT
 384
 Val Glu Val Asn Lys Ser Leu His Ile Thr Cys Lys Asn Pro Asn Tyr
 115 120 125
 GAA GAG CTG ATC CAG GAC ACA TGG CTG TAT AAG AAC TGT AAG GAA ATA
 432
 Glu Glu Leu Ile Gln Asp Thr Trp Leu Tyr Lys Asn Cys Lys Glu Ile
 130 135 140
 TCC AAA ACC CCA AGG ATC CTG AAG GAT GCC GAG TTT GGA GAT GAG GGC
 480
 Ser Lys Thr Pro Arg Ile Leu Lys Asp Ala Glu Phe Gly Asp Glu Gly
 145 150 155 160
 TAC TAC TCC TGC GTG TTT TCT GTC CAC CAT AAT GGG ACA CGG TAC AAC
 528
 Tyr Tyr Ser Cys Val Phe Ser Val His His Asn Gly Thr Arg Tyr Asn

5 ATC ACC AAG ACT 165 GTC AAT ATA ACA GTT 170 ATT GAA GGA AGG AGT 175 AAA GTA
 576
 Ile Thr Lys Thr Val Asn Ile Thr Val Ile Glu Gly Arg Ser Lys Val
 180 185 190
 ACT CCA GCT ATT TTA GGA CCA AAG TGT GAG AAG GTT GGT GTA GAA CTA
 624
 Thr Pro Ala Ile Leu Gly Pro Lys Cys Glu Lys Val Gly Val Glu Leu
 195 200 205
 10 GGA AAG GAT GTG GAG TTG AAC TGC AGT GCT TCA TTG AAT AAA GAC GAT
 672
 Gly Lys Asp Val Glu Leu Asn Cys Ser Ala Ser Leu Asn Lys Asp Asp
 210 215 220
 CTG TTT TAT TGG AGC ATC AGG AAA GAG GAC AGC TCA GAC CCT AAT GTG
 720
 15 Leu Phe Tyr Trp Ser Ile Arg Lys Glu Asp Ser Ser Asp Pro Asn Val
 225 230 235 240
 CAA GAA GAC AGG AAG GAG ACG ACA ACA TGG ATT TCT GAA GGC AAA CTG
 768
 Gln Glu Asp Arg Lys Glu Thr Thr Thr Trp Ile Ser Glu Gly Lys Leu
 245 250 255
 20 CAT GCT TCA AAA ATA CTG AGA TTT CAG AAA ATT ACT GAA AAC TAT CTC
 816
 His Ala Ser Lys Ile Leu Arg Phe Gln Lys Ile Thr Glu Asn Tyr Leu
 260 265 270
 AAT GTT TTA TAT AAT TGC ACC GTG GCC AAC GAA GAA GCC ATA GAC ACC
 864
 25 Asn Val Leu Tyr Asn Cys Thr Val Ala Asn Glu Glu Ala Ile Asp Thr
 275 280 285
 AAG AGC TTC GTC TTG GTG AGA AAA GAA ATA CCT GAT ATC CCA GGC CAT
 912
 Lys Ser Phe Val Leu Val Arg Lys Glu Ile Pro Asp Ile Pro Gly His
 290 295 300
 30 GTC TTT ACA
 921
 Val Phe Thr
 305

(6) INFORMATION FOR SEQ ID NO:5:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 621 base pairs
 (B) TYPE: nucleic acid
 (C) strandedness: double
 (D) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: cDNA
 (ix) FEATURE:
 (A) NAME/KEY: mat peptide
 (B) LOCATION: 1..621
 (C) IDENTIFICATION METHOD: S
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

45 GAA TCT TGT ACT TCA CGT CCC CAC ATT ACT GTG GTT GAA GGG GAA CCT
 48
 Glu Ser Cys Thr Ser Arg Pro His Ile Thr Val Val Glu Gly Glu Pro
 1 5 10 15
 TTC TAT CTG AAA CAT TGC TCG TGT TCA CTT GCA CAT GAG ATT GAA ACA
 96
 50 Phe Tyr Leu Lys His Cys Ser Cys Ser Leu Ala His Glu Ile Glu Thr
 20 25 30
 ACC ACC AAA AGC TGG TAC AAA AGC AGT GGA TCA CAG GAA CAT GTG GAG
 144

Thr Thr Lys Ser Trp Tyr Lys Ser Ser Gly Ser Gln Glu His Val Glu
 35 40 45
 CTG AAC CCA AGG AGT TCC TCG AGA ATT GCT TTG CAT GAT TGT GTT TTG
 192
 5 Leu Asn Pro Arg Ser Ser Ser Arg Ile Ala Leu His Asp Cys Val Leu
 50 55 60
 GAG TTT TGG CCA GTT GAG TTG AAT GAC ACA GGA TCT TAC TTT TTC CAA
 240
 10 Glu Phe Trp Pro Val Glu Leu Asn Asp Thr Gly Ser Tyr Phe Phe Gln
 65 70 75 80
 ATG AAA AAT TAT ACT CAG AAA TGG AAA TTA AAT GTC ATC AGA AGA AAT
 288
 Met Lys Asn Tyr Thr Gln Lys Trp Lys Leu Asn Val Ile Arg Arg Asn
 85 90 95
 AAA CAC AGC TGT TTC ACT GAA AGA CAA GTA ACT AGT AAA ATT GTG GAA
 336
 15 Lys His Ser Cys Phe Thr Glu Arg Gln Val Thr Ser Lys Ile Val Glu
 100 105 110
 GTT AAA AAA TTT TTT CAG ATA ACC TGT GAA AAC AGT TAC TAT CAA ACA
 384
 20 Val Lys Lys Phe Phe Gln Ile Thr Cys Glu Asn Ser Tyr Tyr Gln Thr
 115 120 125
 CTG GTC AAC AGC ACA TCA TTG TAT AAG AAC TGT AAA AAG CTA CTA CTG
 432
 Leu Val Asn Ser Thr Ser Leu Tyr Lys Asn Cys Lys Lys Leu Leu Leu
 130 135 140
 25 GAG AAC AAT AAA AAC CCA ACG ATA AAG AAG AAC GCC GAG TTT GAA GAT
 480
 Glu Asn Asn Lys Asn Pro Thr Ile Lys Lys Asn Ala Glu Phe Glu Asp
 145 150 155 160
 GAG GGG TAT TAC TCC TGC GTG CAT TTC CTT CAT CAT AAT GGA AAA CTA
 528
 30 Gln Gly Tyr Tyr Ser Cys Val His Phe Leu His His Asn Gly Lys Leu
 165 170 175
 TTT AAT ATC ACC AAA ACC TTC AAT ATA ACA ATA GTG GAA GAT CGC AGT
 576
 Phe Asn Ile Thr Lys Thr Phe Asn Ile Thr Ile Val Glu Asp Arg Ser
 180 185 190
 AAT ATA GTT CCG GTT CTT CTT GGA CCA AAG CTT AAC CAT GTT GCA
 621
 35 Asn Ile Val Pro Val Leu Leu Gly Pro Lys Leu Asn His Val Ala
 195 200 205

(7) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 927 base pairs

(B) TYPE: nucleic acid

(C) strandedness: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: mat peptide

(B) LOCATION: 1..927

(C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAA TCT TGT ACT TCA CGT CCC CAC ATT ACT GTG GTT GAA GGG GAA CCT
 48
 50 Glu Ser Cys Thr Ser Arg Pro His Ile Thr Val Val Glu Gly Glu Pro
 1 5 10 15
 TTC TAT CTG AAA CAT TGC TCG TGT TCA CTT GCA CAT GAG ATT GAA ACA

EP 0 864 585 A1

96
Phe Tyr Leu Lys His Cys Ser Cys Ser Leu Ala His Glu Ile Glu Thr
20 25 30
5 ACC ACC AAA AGC TGG TAC AAA AGC AGT GGA TCA CAG GAA CAT GTG GAG
144
Thr Thr Lys Ser Trp Tyr Lys Ser Ser Gly Ser Gln Glu His Val Glu
35 40 45
CTG AAC CCA AGG AGT TCC TCG AGA ATT GCT TTG CAT GAT TGT GTT TTG
192
10 Leu Asn Pro Arg Ser Ser Ser Arg Ile Ala Leu His Asp Cys Val Leu
50 55 60
GAG TTT TGG CCA GTT GAG TTG AAT GAC ACA GGA TCT TAC TTT TTC CAA
240
Glu Phe Trp Pro Val Glu Leu Asn Asp Thr Gly Ser Tyr Phe Phe Gln
65 70 75 80
15 ATG AAA AAT TAT ACT CAG AAA TGG AAA TTA AAT GTC ATC AGA AGA AAT
288
Met Lys Asn Tyr Thr Gln Lys Trp Lys Leu Asn Val Ile Arg Arg Asn
85 90 95
AAA CAC AGC TGT TTC ACT GAA AGA CAA GTA ACT AGT AAA ATT GTG GAA
336
20 Lys His Ser Cys Phe Thr Glu Arg Gln Val Thr Ser Lys Ile Val Glu
100 105 110
GTT AAA AAA TTT TTT CAG ATA ACC TGT GAA AAC AGT TAC TAT CAA ACA
384
Val Lys Lys Phe Phe Gln Ile Thr Cys Glu Asn Ser Tyr Tyr Gln Thr
115 120 125
25 CTG GTC AAC AGC ACA TCA TTG TAT AAG AAC TGT AAA AAG CTA CTA CTG
432
Leu Val Asn Ser Thr Ser Leu Tyr Lys Asn Cys Lys Lys Leu Leu Leu
130 135 140
GAG AAC AAT AAA AAC CCA ACG ATA AAG AAG AAC GCC GAG TTT GAA GAT
480
30 Glu Asn Asn Lys Asn Pro Thr Ile Lys Lys Asn Ala Glu Phe Glu Asp
145 150 155 160
CAG GGG TAT TAC TCC TGC GTG CAT TTC CTT CAT CAT AAT GGA AAA CTA
528
Gln Gly Tyr Tyr Ser Cys Val His Phe Leu His His Asn Gly Lys Leu
165 170 175
35 TTT AAT ATC ACC AAA ACC TTC AAT ATA ACA ATA GTG GAA GAT CGC AGT
576
Phe Asn Ile Thr Lys Thr Phe Asn Ile Thr Ile Val Glu Asp Arg Ser
180 185 190
AAT ATA GTT CCG GTT CTT CTT GGA CCA AAG CTT AAC CAT GTT GCA GTG
624
40 Asn Ile Val Pro Val Leu Leu Gly Pro Lys Leu Asn His Val Ala Val
195 200 205
GAA TTA GGA AAA AAC GTA AGG CTC AAC TGC TCT GCT TTG CTG AAT GAA
672
Glu Leu Gly Lys Asn Val Arg Leu Asn Cys Ser Ala Leu Leu Asn Glu
210 215 220
45 GAG GAT GTA ATT TAT TGG ATG TTC GGG GAA GAA AAT GGA TCG GAT CCT
720
Glu Asp Val Ile Tyr Trp Met Phe Gly Glu Glu Asn Gly Ser Asp Pro
225 230 235 240
AAT ATA CAT GAA GAG AAA GAA ATG AGA ATT ATG ACT CCA GAA GGC AAA
768
50 Asn Ile His Glu Glu Lys Glu Met Arg Ile Met Thr Pro Glu Gly Lys
245 250 255
TGG CAT GCT TCA AAA GTA TTG AGA ATT GAA AAT ATT GGT GAA AGC AAT
816

55

5 Trp His Ala Ser Lys Val Leu Arg Ile Glu Asn Ile Gly Glu Ser Asn
 260 265 270
 CTA AAT GTT TTA TAT AAT TGC ACT GTG GCC AGC ACG GGA GGC ACA GAC
 864
 Leu Asn Val Leu Tyr Asn Cys Thr Val Ala Ser Thr Gly Gly Thr Asp
 275 280 285
 ACC AAA AGC TTC ATC TTG GTG AGA AAA GAC ATG GCT GAT ATC CCA GGC
 912
 10 Thr Lys Ser Phe Ile Leu Val Arg Lys Asp Met Ala Asp Ile Pro Gly
 290 295 300
 CAC GTC TTC ACA AGA
 927
 His Val Phe Thr Arg
 305

15 (8) INFORMATION FOR SEQ ID NO:7:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH:1620 base pairs
 (B) TYPE:nucleic acid
 (C) strandedness:double
 (D) TOPOLOGY:linear
 20 (ii) MOLECULE TYPE:cDNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM:lymphoblastoid cell derived from a patient
 with Hodgkin's disease
 (B) INDIVIDUAL ISOLATE:L428 (FERM BP-5777)
 (ix) FEATURE:
 25 (A) NAME/KEY:sig peptide
 (B) LOCATION:1..57
 (C) IDENTIFICATION METHOD:E
 (ix) FEATURE:
 (A) NAME/KEY:mat peptide
 (B) LOCATION:58..1620
 30 (C) IDENTIFICATION METHOD:E
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:7:

ATG AAT TGT AGA GAA TTA CCC TTG ACC CTT TGG GTG CTT ATA TCT GTA
 48
 Met Asn Cys Arg Glu Leu Pro Leu Thr Leu Trp Val Leu Ile Ser Val
 35 -15 -10 -5
 AGC ACT GCA GAA TCT TGT ACT TCA CGT CCC CAC ATT ACT GTG GTT GAA
 96
 Ser Thr Ala Glu Ser Cys Thr Ser Arg Pro His Ile Thr Val Val Glu
 1 5 10
 GGG GAA CCT TTC TAT CTG AAA CAT TGC TCG TGT TCA CTT GCA CAT GAG
 144
 40 Gly Glu Pro Phe Tyr Leu Lys His Cys Ser Cys Ser Leu Ala His Glu
 15 20 25
 ATT GAA ACA ACC ACC AAA AGC TGG TAC AAA AGC AGT GGA TCA CAG GAA
 192
 Ile Glu Thr Thr Thr Lys Ser Trp Tyr Lys Ser Ser Gly Ser Gln Glu
 30 35 40 45
 45 CAT GTG GAG CTG AAC CCA AGG AGT TCC TCG AGA ATT GCT TTG CAT GAT
 240
 His Val Glu Leu Asn Pro Arg Ser Ser Ser Arg Ile Ala Leu His Asp
 50 55 60
 TGT GTT TTG GAG TTT TGG CCA GTT GAG TTG AAT GAC ACA GGA TCT TAC
 288
 50 Cys Val Leu Glu Phe Trp Pro Val Glu Leu Asn Asp Thr Gly Ser Tyr
 65 70 75
 TTT TTC CAA ATG AAA AAT TAT ACT CAG AAA TGG AAA TTA AAT GTC ATC

55

336
 Phe Phe Gln Met Lys Asn Tyr Thr Gln Lys Trp Lys Leu Asn Val Ile
 80 85 90
 5 AGA AGA AAT AAA CAC AGC TGT TTC ACT GAA AGA CAA GTA ACT AGT AAA
 384
 Arg Arg Asn Lys His Ser Cys Phe Thr Glu Arg Gln Val Thr Ser Lys
 95 100 105
 ATT GTG GAA GTT AAA AAA TTT TTT CAG ATA ACC TGT GAA AAC AGT TAC
 432
 10 Ile Val Glu Val Lys Lys Phe Phe Gln Ile Thr Cys Glu Asn Ser Tyr
 110 115 120 125
 TAT CAA ACA CTG GTC AAC AGC ACA TCA TTG TAT AAG AAC TGT AAA AAG
 480
 Tyr Gln Thr Leu Val Asn Ser Thr Ser Leu Tyr Lys Asn Cys Lys Lys
 130 135 140
 15 CTA CTA CTG GAG AAC AAT AAA AAC CCA ACG ATA AAG AAG AAC GCC GAG
 528
 Leu Leu Leu Glu Asn Asn Lys Asn Pro Thr Ile Lys Lys Asn Ala Glu
 145 150 155
 TTT GAA GAT CAG GGG TAT TAC TCC TGC GTG CAT TTC CTT CAT CAT AAT
 576
 20 Phe Glu Asp Gln Gly Tyr Tyr Ser Cys Val His Phe Leu His His Asn
 160 165 170
 GGA AAA CTA TTT AAT ATC ACC AAA ACC TTC AAT ATA ACA ATA GTG GAA
 624
 Gly Lys Leu Phe Asn Ile Thr Lys Thr Phe Asn Ile Thr Ile Val Glu
 175 180 185
 25 GAT CGC AGT AAT ATA GTT CCG GTT CTT CTT GGA CCA AAG CTT AAC CAT
 672
 Asp Arg Ser Asn Ile Val Pro Val Leu Leu Gly Pro Lys Leu Asn His
 190 195 200 205
 GTT GCA GTG GAA TTA GGA AAA AAC GTA AGG CTC AAC TGC TCT GCT TTG
 720
 30 Val Ala Val Glu Leu Gly Lys Asn Val Arg Leu Asn Cys Ser Ala Leu
 210 215 220
 CTG AAT GAA GAG GAT GTA ATT TAT TGG ATG TTC GGG GAA GAA AAT GGA
 768
 Leu Asn Glu Glu Asp Val Ile Tyr Trp Met Phe Gly Glu Glu Asn Gly
 225 230 235
 35 TCG GAT CCT AAT ATA CAT GAA GAG AAA GAA ATG AGA ATT ATG ACT CCA
 816
 Ser Asp Pro Asn Ile His Glu Glu Lys Glu Met Arg Ile Met Thr Pro
 240 245 250
 GAA GGC AAA TGG CAT GCT TCA AAA GTA TTG AGA ATT GAA AAT ATT GGT
 864
 40 Glu Gly Lys Trp His Ala Ser Lys Val Leu Arg Ile Glu Asn Ile Gly
 255 260 265
 GAA AGC AAT CTA AAT GTT TTA TAT AAT TGC ACT GTG GCC AGC ACG GGA
 912
 Glu Ser Asn Leu Asn Val Leu Tyr Asn Cys Thr Val Ala Ser Thr Gly
 270 275 280 285
 45 GGC ACA GAC ACC AAA AGC TTC ATC TTG GTG AGA AAA GAC ATG GCT GAT
 960
 Gly Thr Asp Thr Lys Ser Phe Ile Leu Val Arg Lys Asp Met Ala Asp
 290 295 300
 ATC CCA GGC CAC GTC TTC ACA AGA GGA ATG ATC ATA GCT GTT TTG ATC
 1008
 50 Ile Pro Gly His Val Phe Thr Arg Gly Met Ile Ile Ala Val Leu Ile
 305 310 315
 TTG GTG GCA GTA GTG TGC CTA GTG ACT GTG TGT GTC ATT TAT AGA GTT
 1056

5 Leu Val Ala Val Val Cys Leu Val Thr Val Cys Val Ile Tyr Arg Val
 320 325 330
 GAC TTG GTT CTA TTT TAT AGA CAT TTA ACG AGA AGA GAT GAA ACA TTA
 1104
 Asp Leu Val Leu Phe Tyr Arg His Leu Thr Arg Arg Asp Glu Thr Leu
 335 340 345
 ACA GAT GGA AAA ACA TAT GAT GCT TTT GTG TCT TAC CTA AAA GAA TGC
 1152
 10 Thr Asp Gly Lys Thr Tyr Asp Ala Phe Val Ser Tyr Leu Lys Glu Cys
 350 355 360 365
 CGA CCT GAA AAT GGA GAG GAG CAC ACC TTT GCT GTG GAG ATT TTG CCC
 1200
 Arg Pro Glu Asn Gly Glu Glu His Thr Phe Ala Val Glu Ile Leu Pro
 370 375 380
 15 AGG GTG TTG GAG AAA CAT TTT GGG TAT AAG TTA TGC ATA TTT GAA AGG
 1248
 Arg Val Leu Glu Lys His Phe Gly Tyr Lys Leu Cys Ile Phe Glu Arg
 385 390 395
 GAT GTA GTG CCT GGA GGA GCT GTT GTT GAT GAA ATC CAC TCA CTG ATA
 1296
 20 Asp Val Val Pro Gly Gly Ala Val Val Asp Glu Ile His Ser Leu Ile
 400 405 410
 GAG AAA AGC CGA AGA CTA ATC ATT GTC CTA AGT AAA AGT TAT ATG TCT
 1344
 Glu Lys Ser Arg Arg Leu Ile Ile Val Leu Ser Lys Ser Tyr Met Ser
 415 420 425
 25 AAT GAG GTC AGG TAT GAA CTT GAA AGT GGA CTC CAT GAA GCA TTG GTG
 1392
 Asn Glu Val Arg Tyr Glu Leu Glu Ser Gly Leu His Glu Ala Leu Val
 430 435 440 445
 GAA AGA AAA ATT AAA ATA ATC TTA ATT GAA TTT ACA CCT GTT ACT GAC
 1440
 30 Glu Arg Lys Ile Lys Ile Ile Leu Ile Glu Phe Thr Pro Val Thr Asp
 450 455 460
 TTC ACA TTC TTG CCC CAA TCA CTA AAG CTT TTG AAA TCT CAC AGA GTT
 1488
 Phe Thr Phe Leu Pro Gln Ser Leu Lys Leu Leu Lys Ser His Arg Val
 465 470 475
 35 CTG AAG TGG AAG GCC GAT AAA TCT CTT TCT TAT AAC TCA AGG TTC TGG
 1536
 Leu Lys Trp Lys Ala Asp Lys Ser Leu Ser Tyr Asn Ser Arg Phe Trp
 480 485 490
 AAG AAC CTT CTT TAC TTA ATG CCT GCA AAA ACA GTC AAG CCA GGT AGA
 1584
 40 Lys Asn Leu Leu Tyr Leu Met Pro Ala Lys Thr Val Lys Pro Gly Arg
 495 500 505
 GAC GAA CCG GAA GTC TTG CCT GTT CTT TCC GAG TCT
 1620
 Asp Glu Pro Glu Val Leu Pro Val Leu Ser Glu Ser
 510 515 520

(9) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 base pairs

(B) TYPE: nucleic acid

(C) strandedness: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION:1..57
(C) IDENTIFICATION METHOD:S

(ix) FEATURE:

(A) NAME/KEY:mat peptide

(B) LOCATION:58..369

(C) IDENTIFICATION METHOD:S

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:8:

ATG AAT TGT AGA GAA TTA CCC TTG ACC CTT TGG GTG CTT ATA TCT GTA
48
Met Asn Cys Arg Glu Leu Pro Leu Thr Leu Trp Val Leu Ile Ser Val
-15 -10 -5
AGC ACT GCA GAA TCT TGT ACT TCA CGT CCC CAC ATT ACT GTG GTT GAA
96
Ser Thr Ala Glu Ser Cys Thr Ser Arg Pro His Ile Thr Val Val Glu
1 5 10
GGG GAA CCT TTC TAT CTG AAA CAT TGC TCG TGT TCA CTT GCA CAT GAG
144
Gly Glu Pro Phe Tyr Leu Lys His Cys Ser Cys Ser Leu Ala His Glu
15 20 25
ATT GAA ACA ACC ACC AAA AGC TGG TAC AAA AGC AGT GGA TCA CAG GAA
192
Ile Glu Thr Thr Thr Lys Ser Trp Tyr Lys Ser Ser Gly Ser Gln Glu
30 35 40 45
CAT GTG GAG CTG AAC CCA AGG AGT TCC TCG AGA ATT GCT TTG CAT GAT
240
His Val Glu Leu Asn Pro Arg Ser Ser Ser Arg Ile Ala Leu His Asp
50 55 60
TGT GTT TTG GAG TTT TGG CCA GTT GAG TTG AAT GAC ACA GGA TCT TAC
288
Cys Val Leu Glu Phe Trp Pro Val Glu Leu Asn Asp Thr Gly Ser Tyr
65 70 75
TTT TTC CAA ATG AAA AAT TAT ACT CAG AAA TGG AAA TTA AAT GTC ATC
336
Phe Phe Gln Met Lys Asn Tyr Thr Gln Lys Trp Lys Leu Asn Val Ile
80 85 90
AGA AGA AAT AAA CAC AGC TGT TTC ACT GAA AGA
369
Arg Arg Asn Lys His Ser Cys Phe Thr Glu Arg
95 100

(10) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:678 base pairs

(B) TYPE:nucleic acid

(C) strandedness:double

(D) TOPOLOGY:linear

(ii) MOLECULE TYPE:cDNA

(ix) FEATURE:

(A) NAME/KEY:sig peptide

(B) LOCATION:1..57

(C) IDENTIFICATION METHOD:S

(ix) FEATURE:

(A) NAME/KEY:mat peptide

(B) LOCATION:58..678

(C) IDENTIFICATION METHOD:S

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:9:

ATG AAT TGT AGA GAA TTA CCC TTG ACC CTT TGG GTG CTT ATA TCT GTA
48
Met Asn Cys Arg Glu Leu Pro Leu Thr Leu Trp Val Leu Ile Ser Val

EP 0 864 585 A1

				-15					-10					-5		
	AGC	ACT	GCA	GAA	TCT	TGT	ACT	TCA	CGT	CCC	CAC	ATT	ACT	GTG	GTT	GAA
5	96	Ser	Thr	Ala	Glu	Ser	Cys	Thr	Ser	Arg	Pro	His	Ile	Thr	Val	Val
				1				5					10			
	GGG	GAA	CCT	TTC	TAT	CTG	AAA	CAT	TGC	TCG	TGT	TCA	CTT	GCA	CAT	GAG
	144	Gly	Glu	Pro	Phe	Tyr	Leu	Lys	His	Cys	Ser	Cys	Ser	Leu	Ala	His
		15					20				25					
10	ATT	GAA	ACA	ACC	ACC	AAA	AGC	TGG	TAC	AAA	AGC	AGT	GGA	TCA	CAG	GAA
	192	Ile	Glu	Thr	Thr	Thr	Lys	Ser	Trp	Tyr	Lys	Ser	Ser	Gly	Ser	Gln
		30				35				40						45
	CAT	GTG	GAG	CTG	AAC	CCA	AGG	AGT	TCC	TCG	AGA	ATT	GCT	TTG	CAT	GAT
	240	His	Val	Glu	Leu	Asn	Pro	Arg	Ser	Ser	Arg	Ile	Ala	Leu	His	Asp
15					50					55					60	
	TGT	GTT	TTG	GAG	TTT	TGG	CCA	GTT	GAG	TTG	AAT	GAC	ACA	GGA	TCT	TAC
	288	Cys	Val	Leu	Glu	Phe	Trp	Pro	Val	Glu	Leu	Asn	Asp	Thr	Gly	Ser
				65				70				75				
20	TTT	TTC	CAA	ATG	AAA	AAT	TAT	ACT	CAG	AAA	TGG	AAA	TTA	AAT	GTC	ATC
	336	Phe	Phe	Gln	Met	Lys	Asn	Tyr	Thr	Gln	Lys	Trp	Lys	Leu	Asn	Val
				80				85				90				
	AGA	AGA	AAT	AAA	CAC	AGC	TGT	TTC	ACT	GAA	AGA	CAA	GTA	ACT	AGT	AAA
	384	Arg	Arg	Asn	Lys	His	Ser	Cys	Phe	Thr	Glu	Arg	Gln	Val	Thr	Ser
25								100				105				
	ATT	GTG	GAA	GTT	AAA	AAA	TTT	TTT	CAG	ATA	ACC	TGT	GAA	AAC	AGT	TAC
	432	Ile	Val	Glu	Val	Lys	Lys	Phe	Phe	Gln	Ile	Thr	Cys	Glu	Asn	Ser
						115					120					125
30	TAT	CAA	ACA	CTG	GTC	AAC	AGC	ACA	TCA	TTG	TAT	AAG	AAC	TGT	AAA	AAG
	480	Tyr	Gln	Thr	Leu	Val	Asn	Ser	Thr	Ser	Leu	Tyr	Lys	Asn	Cys	Lys
					130					135				140		
	CTA	CTA	CTG	GAG	AAC	AAT	AAA	AAC	CCA	ACG	ATA	AAG	AAG	AAC	GCC	GAG
	528	Leu	Leu	Leu	Glu	Asn	Asn	Lys	Asn	Pro	Thr	Ile	Lys	Lys	Asn	Ala
35				145				150					155			
	TTT	GAA	GAT	CAG	GGG	TAT	TAC	TCC	TGC	GTG	CAT	TTC	CTT	CAT	CAT	AAT
	576	Phe	Glu	Asp	Gln	Gly	Tyr	Tyr	Ser	Cys	Val	His	Phe	Leu	His	His
			160					165				170				
40	GGA	AAA	CTA	TTT	AAT	ATC	ACC	AAA	ACC	TTC	AAT	ATA	ACA	ATA	GTG	GAA
	624	Gly	Lys	Leu	Phe	Asn	Ile	Thr	Lys	Thr	Phe	Asn	Ile	Thr	Ile	Val
			175			180					185					
	GAT	CGC	AGT	AAT	ATA	GTT	CCG	GTT	CTT	CTT	GGA	CCA	AAG	CTT	AAC	CAT
	672	Asp	Arg	Ser	Asn	Ile	Val	Pro	Val	Leu	Leu	Gly	Pro	Lys	Leu	Asn
45					195					200						205
	GTT	GCA														
	678	Val	Ala													

(11) INFORMATION FOR SEQ ID NO:10:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 984 base pairs
 (B) TYPE: nucleic acid

55

(C) strandedness:double
 (D) TOPOLOGY:linear
 (ii) MOLECULE TYPE:cDNA
 (ix) FEATURE:
 (A) NAME/KEY:sig peptide
 (B) LOCATION:1..57
 (C) IDENTIFICATION METHOD:E
 (ix) FEATURE:
 (A) NAME/KEY:mat peptide
 (B) LOCATION:58..984
 (C) IDENTIFICATION METHOD:E
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:10:

ATG AAT TGT AGA GAA TTA CCC TTG ACC CTT TGG GTG CTT ATA TCT GTA
 48
 Met Asn Cys Arg Glu Leu Pro Leu Thr Leu Trp Val Leu Ile Ser Val
 -15 -10 -5
 AGC ACT GCA GAA TCT TGT ACT TCA CGT CCC CAC ATT ACT GTG GTT GAA
 96
 Ser Thr Ala Glu Ser Cys Thr Ser Arg Pro His Ile Thr Val Val Glu
 1 5 10
 GGG GAA CCT TTC TAT CTG AAA CAT TGC TCG TGT TCA CTT GCA CAT GAG
 144
 Gly Glu Pro Phe Tyr Leu Lys His Cys Ser Cys Ser Leu Ala His Glu
 15 20 25
 ATT GAA ACA ACC ACC AAA AGC TGG TAC AAA AGC AGT GGA TCA CAG GAA
 192
 Ile Glu Thr Thr Thr Lys Ser Trp Tyr Lys Ser Ser Gly Ser Gln Glu
 30 35 40 45
 CAT GTG GAG CTG AAC CCA AGG AGT TCC TCG AGA ATT GCT TTG CAT GAT
 240
 His Val Glu Leu Asn Pro Arg Ser Ser Ser Arg Ile Ala Leu His Asp
 50 55 60
 TGT GTT TTG GAG TTT TGG CCA GTT GAG TTG AAT GAC ACA GGA TCT TAC
 288
 Cys Val Leu Glu Phe Trp Pro Val Glu Leu Asn Asp Thr Gly Ser Tyr
 65 70 75
 TTT TTC CAA ATG AAA AAT TAT ACT CAG AAA TGG AAA TTA AAT GTC ATC
 336
 Phe Phe Gln Met Lys Asn Tyr Thr Gln Lys Trp Lys Leu Asn Val Ile
 80 85 90
 AGA AGA AAT AAA CAC AGC TGT TTC ACT GAA AGA CAA GTA ACT AGT AAA
 384
 Arg Arg Asn Lys His Ser Cys Phe Thr Glu Arg Gln Val Thr Ser Lys
 95 100 105
 ATT GTG GAA GTT AAA AAA TTT TTT CAG ATA ACC TGT GAA AAC AGT TAC
 432
 Ile Val Glu Val Lys Lys Phe Phe Gln Ile Thr Cys Glu Asn Ser Tyr
 110 115 120 125
 TAT CAA ACA CTG GTC AAC AGC ACA TCA TTG TAT AAG AAC TGT AAA AAG
 480
 Tyr Gln Thr Leu Val Asn Ser Thr Ser Leu Tyr Lys Asn Cys Lys Lys
 130 135 140
 CTA CTA CTG GAG AAC AAT AAA AAC CCA ACG ATA AAG AAG AAC GCC GAG
 528
 Leu Leu Leu Glu Asn Asn Lys Asn Pro Thr Ile Lys Lys Asn Ala Glu
 145 150 155
 TTT GAA GAT CAG GGG TAT TAC TCC TGC GTG CAT TTC CTT CAT CAT AAT
 576
 Phe Glu Asp Gln Gly Tyr Tyr Ser Cys Val His Phe Leu His His Asn
 160 165 170

5 GGA AAA CTA TTT AAT ATC ACC AAA ACC TTC AAT ATA ACA ATA GTG GAA
 624
 Gly Lys Leu Phe Asn Ile Thr Lys Thr Phe Asn Ile Thr Ile Val Glu
 175 180 185
 10 GAT CGC AGT AAT ATA GTT CCG GTT CTT CTT GGA CCA AAG CTT AAC CAT
 672
 Asp Arg Ser Asn Ile Val Pro Val Leu Leu Gly Pro Lys Leu Asn His
 190 195 200 205
 GTT GCA GTG GAA TTA GGA AAA AAC GTA AGG CTC AAC TGC TCT GCT TTG
 720
 Val Ala Val Glu Leu Gly Lys Asn Val Arg Leu Asn Cys Ser Ala Leu
 210 215 220
 15 CTG AAT GAA GAG GAT GTA ATT TAT TGG ATG TTC GGG GAA GAA AAT GGA
 768
 Leu Asn Glu Glu Asp Val Ile Tyr Trp Met Phe Gly Glu Glu Asn Gly
 225 230 235
 TCG GAT CCT AAT ATA CAT GAA GAG AAA GAA ATG AGA ATT ATG ACT CCA
 816
 Ser Asp Pro Asn Ile His Glu Glu Lys Glu Met Arg Ile Met Thr Pro
 240 245 250
 20 GAA GGC AAA TGG CAT GCT TCA AAA GTA TTG AGA ATT GAA AAT ATT GGT
 864
 Glu Gly Lys Trp His Ala Ser Lys Val Leu Arg Ile Glu Asn Ile Gly
 255 260 265
 GAA AGC AAT CTA AAT GTT TTA TAT AAT TGC ACT GTG GCC AGC ACG GGA
 912
 25 Glu Ser Asn Leu Asn Val Leu Tyr Asn Cys Thr Val Ala Ser Thr Gly
 270 275 280 285
 GGC ACA GAC ACC AAA AGC TTC ATC TTG GTG AGA AAA GAC ATG GCT GAT
 960
 Gly Thr Asp Thr Lys Ser Phe Ile Leu Val Arg Lys Asp Met Ala Asp
 290 295 300
 30 ATC CCA GGC CAC GTC TTC ACA AGA
 984
 Ile Pro Gly His Val Phe Thr Arg
 305

(12) INFORMATION FOR SEQ ID NO:11:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 975 base pairs
 (B) TYPE: nucleic acid
 (C) strandedness: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (ix) FEATURE:
 40 (A) NAME/KEY: sig peptide
 (B) LOCATION: 1..54
 (C) IDENTIFICATION METHOD: S
 (ix) FEATURE:
 (A) NAME/KEY: mat peptide
 (B) LOCATION: 55..975
 (C) IDENTIFICATION METHOD: S
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

50 ATG CAT CAT GAA GAA TTA ATC TTG ACA CTC TGC ATT CTC ATT GTT AAA
 48
 Met His His Glu Glu Leu Ile Leu Thr Leu Cys Ile Leu Ile Val Lys
 -15 -10 -5
 AGT GCC TCA AAA AGT TGT ATT CAC CGA TCA CAA ATT CAT GTG GTA GAG
 96
 Ser Ala Ser Lys Ser Cys Ile His Arg Ser Gln Ile His Val Val Glu

55

1 5 10
 GGA GAA CCT TTT TAT CTG AAG CCA TGT GGC ATA TCT GCA CCA GTG CAC
 144
 5 Gly Glu Pro Phe Tyr Leu Lys Pro Cys Gly Ile Ser Ala Pro Val His
 15 20 25 30
 AGG AAT GAA ACA GCC ACC ATG AGA TGG TTC AAA GGC AGT GCT TCA CAT
 192
 Arg Asn Glu Thr Ala Thr Met Arg Trp Phe Lys Gly Ser Ala Ser His
 35 40 45
 10 GAG TAT AGA GAG CTG AAC AAC AGA AGC TCG CCC AGA GTC ACT TTT CAT
 240
 Glu Tyr Arg Glu Leu Asn Asn Arg Ser Ser Pro Arg Val Thr Phe His
 50 55 60
 GAT CAC ACC TTG GAA TTC TGG CCA GTT GAG ATG GAG GAT GAG GGA ACG
 288
 15 Asp His Thr Leu Glu Phe Trp Pro Val Glu Met Glu Asp Glu Gly Thr
 65 70 75
 TAC ATT TCT CAA GTC GGA AAT GAT CGT CGC AAT TGG ACC TTA AAT GTC
 336
 Tyr Ile Ser Gln Val Gly Asn Asp Arg Arg Asn Trp Thr Leu Asn Val
 80 85 90
 20 ACC AAA AGA AAC AAA CAC AGC TGT TTC TCT GAC AAG CTC GTG ACA AGC
 384
 Thr Lys Arg Asn Lys His Ser Cys Phe Ser Asp Lys Leu Val Thr Ser
 95 100 105
 AGA GAT GTT GAA GTT AAC AAA TCT CTG CAT ATC ACT TGT AAG AAT CCT
 432
 25 Arg Asp Val Glu Val Asn Lys Ser Leu His Ile Thr Cys Lys Asn Pro
 115 120 125
 AAC TAT GAA GAG CTG ATC CAG GAC ACA TGG CTG TAT AAG AAC TGT AAG
 480
 Asn Tyr Glu Glu Leu Ile Gln Asp Thr Trp Leu Tyr Lys Asn Cys Lys
 130 135 140
 30 GAA ATA TCC AAA ACC CCA AGG ATC CTG AAG GAT GCC GAG TTT GGA GAT
 528
 Glu Ile Ser Lys Thr Pro Arg Ile Leu Lys Asp Ala Glu Phe Gly Asp
 145 150 155
 GAG GGC TAC TAC TCC TGC GTG TTT TCT GTC CAC CAT AAT GGG ACA CGG
 576
 35 Glu Gly Tyr Tyr Ser Cys Val Phe Ser Val His His Asn Gly Thr Arg
 160 165 170
 TAC AAC ATC ACC AAG ACT GTC AAT ATA ACA GTT ATT GAA GGA AGG AGT
 624
 Tyr Asn Ile Thr Lys Thr Val Asn Ile Thr Val Ile Glu Gly Arg Ser
 175 180 185
 40 AAA GTA ACT CCA GCT ATT TTA GGA CCA AAG TGT GAG AAG GTT GGT GTA
 672
 Lys Val Thr Pro Ala Ile Leu Gly Pro Lys Cys Glu Lys Val Gly Val
 195 200 205
 GAA CTA GGA AAG GAT GTG GAG TTG AAC TGC AGT GCT TCA TTG AAT AAA
 720
 45 Glu Leu Gly Lys Asp Val Glu Leu Asn Cys Ser Ala Ser Leu Asn Lys
 210 215 220
 GAC GAT CTG TTT TAT TGG AGC ATC AGG AAA GAG GAC AGC TCA GAC CCT
 768
 Asp Asp Leu Phe Tyr Trp Ser Ile Arg Lys Glu Asp Ser Ser Asp Pro
 225 230 235
 50 AAT GTG CAA GAA GAC AGG AAG GAG ACG ACA ACA TGG ATT TCT GAA GGC
 816
 Asn Val Gln Glu Asp Arg Lys Glu Thr Thr Thr Trp Ile Ser Glu Gly
 240 245 250

AAA CTG CAT GCT TCA AAA ATA CTG AGA TTT CAG AAA ATT ACT GAA AAC
 864
 Lys Leu His Ala Ser Lys Ile Leu Arg Phe Gln Lys Ile Thr Glu Asn
 255 260 265 270
 TAT CTC AAT GTT TTA TAT AAT TGC ACC GTG GCC AAC GAA GAA GCC ATA
 912
 Tyr Leu Asn Val Leu Tyr Asn Cys Thr Val Ala Asn Glu Glu Ala Ile
 275 280 285
 GAC ACC AAG AGC TTC GTC TTG GTG AGA AAA GAA ATA CCT GAT ATC CCA
 960
 Asp Thr Lys Ser Phe Val Leu Val Arg Lys Glu Ile Pro Asp Ile Pro
 290 295 300
 GGC CAT GTC TTT ACA
 975
 Gly His Val Phe Thr
 305

(13) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:5

(B) TYPE:amino acid

(D) TOPOLOGY:linear

(ii) MOLECULE TYPE:peptide

(v) FRAGMENT TYPE:internal fragment

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:12:

Trp His Ala Ser Lys
1

(14) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:7

(B) TYPE:amino acid

(D) TOPOLOGY:linear

(ii) MOLECULE TYPE:peptide

(v) FRAGMENT TYPE:internal fragment

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:13:

Ile Met Thr Pro Glu Gly Lys
1 5

(15) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:13

(B) TYPE:amino acid

(D) TOPOLOGY:linear

(ii) MOLECULE TYPE:peptide

(v) FRAGMENT TYPE:internal fragment

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:14:

Ser Ser Gly Ser Gln Glu His Val Glu Leu Asn Pro Arg
1 5 10

(16) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:4

(B) TYPE:amino acid

(D) TOPOLOGY:linear

(ii) MOLECULE TYPE:peptide

(v) FRAGMENT TYPE:internal fragment

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:15:

Ser Trp Tyr Lys
1

5 (17) INFORMATION FOR SEQ ID NO:16:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH:10
 (B) TYPE:amino acid
 (D) TOPOLOGY:linear
 (ii) MOLECULE TYPE:peptide
 10 (v) FRAGMENT TYPE:internal fragment
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:16:

Leu Asn His Val Ala Val Glu Leu Gly Lys
1 5 10

15 (18) INFORMATION FOR SEQ ID NO:17:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH:6
 (B) TYPE:amino acid
 (D) TOPOLOGY:linear
 (ii) MOLECULE TYPE:peptide
 20 (v) FRAGMENT TYPE:internal fragment
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:17:

Ser Phe Ile Leu Val Arg
1 5

25 (19) INFORMATION FOR SEQ ID NO:18:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH:15
 (B) TYPE:amino acid
 (D) TOPOLOGY:linear
 (ii) MOLECULE TYPE:peptide
 30 (v) FRAGMENT TYPE:internal fragment
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:18:

Thr Val Lys Pro Gly Arg Asp Glu Pro Glu Val Leu Pro Val Leu
1 5 10 15

35 (20) INFORMATION FOR SEQ ID NO:19:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH:11
 (B) TYPE:amino acid
 (D) TOPOLOGY:linear
 (ii) MOLECULE TYPE:peptide
 40 (v) FRAGMENT TYPE:internal fragment
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:19:

Ser Asn Ile Val Pro Val Leu Leu Gly Pro Lys
1 5 10

45 (21) INFORMATION FOR SEQ ID NO:20:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH:521
 (B) TYPE:amino acid
 (D) TOPOLOGY:linear
 (ii) MOLECULE TYPE:peptide
 50 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:20:

Glu Ser Cys Thr Ser Arg Pro His Ile Thr Val Val Glu Gly Glu Pro
1 5 10 15

55

EP 0 864 585 A1

	Phe	Tyr	Leu	Lys	His	Cys	Ser	Cys	Ser	Leu	Ala	His	Glu	Ile	Glu	Thr
				20					25					30		
	Thr	Thr	Lys	Ser	Trp	Tyr	Lys	Ser	Ser	Gly	Ser	Gln	Glu	His	Val	Glu
			35					40					45			
5	Leu	Asn	Pro	Arg	Ser	Ser	Ser	Arg	Ile	Ala	Leu	His	Asp	Cys	Val	Leu
		50					55					60				
	Glu	Phe	Trp	Pro	Val	Glu	Leu	Asn	Asp	Thr	Gly	Ser	Tyr	Phe	Phe	Gln
	65					70					75					80
	Met	Lys	Asn	Tyr	Thr	Gln	Lys	Trp	Lys	Leu	Asn	Val	Ile	Arg	Arg	Asn
					85					90					95	
10	Lys	His	Ser	Cys	Phe	Thr	Glu	Arg	Gln	Val	Thr	Ser	Lys	Ile	Val	Glu
				100					105					110		
	Val	Lys	Lys	Phe	Phe	Gln	Ile	Thr	Cys	Glu	Asn	Ser	Tyr	Tyr	Gln	Thr
			115					120					125			
	Leu	Val	Asn	Ser	Thr	Ser	Leu	Tyr	Lys	Asn	Cys	Lys	Lys	Leu	Leu	Leu
		130					135					140				
15	Glu	Asn	Asn	Lys	Asn	Pro	Thr	Ile	Lys	Lys	Asn	Ala	Glu	Phe	Glu	Asp
	145					150					155					160
	Gln	Gly	Tyr	Tyr	Ser	Cys	Val	His	Phe	Leu	His	His	Asn	Gly	Lys	Leu
					165					170					175	
	Phe	Asn	Ile	Thr	Lys	Thr	Phe	Asn	Ile	Thr	Ile	Val	Glu	Asp	Arg	Ser
				180					185					190		
20	Asn	Ile	Val	Pro	Val	Leu	Leu	Gly	Pro	Lys	Leu	Asn	His	Val	Ala	Val
			195					200					205			
	Glu	Leu	Gly	Lys	Asn	Val	Arg	Leu	Asn	Cys	Ser	Ala	Leu	Leu	Asn	Glu
		210					215					220				
	Glu	Asp	Val	Ile	Tyr	Trp	Met	Phe	Gly	Glu	Glu	Asn	Gly	Ser	Asp	Pro
	225					230					235					240
25	Asn	Ile	His	Glu	Glu	Lys	Glu	Met	Arg	Ile	Met	Thr	Pro	Glu	Gly	Lys
					245					250					255	
	Trp	His	Ala	Ser	Lys	Val	Leu	Arg	Ile	Glu	Asn	Ile	Gly	Glu	Ser	Asn
					260				265					270		
	Leu	Asn	Val	Leu	Tyr	Asn	Cys	Thr	Val	Ala	Ser	Thr	Gly	Gly	Thr	Asp
			275					280					285			
30	Thr	Lys	Ser	Phe	Ile	Leu	Val	Arg	Lys	Asp	Met	Ala	Asp	Ile	Pro	Gly
		290					295					300				
	His	Val	Phe	Thr	Arg	Gly	Met	Ile	Ile	Ala	Val	Leu	Ile	Leu	Val	Ala
	305					310					315					320
	Val	Val	Cys	Leu	Val	Thr	Val	Cys	Val	Ile	Tyr	Arg	Val	Asp	Leu	Val
					325					330					335	
35	Leu	Phe	Tyr	Arg	His	Leu	Thr	Arg	Arg	Asp	Glu	Thr	Leu	Thr	Asp	Gly
				340					345					350		
	Lys	Thr	Tyr	Asp	Ala	Phe	Val	Ser	Tyr	Leu	Lys	Glu	Cys	Arg	Pro	Glu
			355					360					365			
	Asn	Gly	Glu	Glu	His	Thr	Phe	Ala	Val	Glu	Ile	Leu	Pro	Arg	Val	Leu
		370					375					380				
40	Glu	Lys	His	Phe	Gly	Tyr	Lys	Leu	Cys	Ile	Phe	Glu	Arg	Asp	Val	Val
	385					390					395					400
	Pro	Gly	Gly	Ala	Val	Val	Asp	Glu	Ile	His	Ser	Leu	Ile	Glu	Lys	Ser
					405					410					415	
	Arg	Arg	Leu	Ile	Ile	Val	Leu	Ser	Lys	Ser	Tyr	Met	Ser	Asn	Glu	Val
				420					425					430		
45	Arg	Tyr	Glu	Leu	Glu	Ser	Gly	Leu	His	Glu	Ala	Leu	Val	Glu	Arg	Lys
			435					440					445			
	Ile	Lys	Ile	Ile	Leu	Ile	Glu	Phe	Thr	Pro	Val	Thr	Asp	Phe	Thr	Phe
		450					455					460				
	Leu	Pro	Gln	Ser	Leu	Lys	Leu	Leu	Lys	Ser	His	Arg	Val	Leu	Lys	Trp
	465					470					475					480
50	Lys	Ala	Asp	Lys	Ser	Leu	Ser	Tyr	Asn	Ser	Arg	Phe	Trp	Lys	Asn	Leu
					485					490					495	
	Leu	Tyr	Leu	Met	Pro	Ala	Lys	Thr	Val	Lys	Pro	Gly	Arg	Asp	Glu	Pro

500
 Glu Val Leu Pro Val Leu Ser Glu Ser 505
 515 520
 510

(22) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 519

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Pro	Phe	Tyr	Leu	Lys	Pro	Cys	Gly	Ile	Ser	Ala	Pro	Val	His	Arg	Asn	
Glu	Thr	Ala	Thr	Met	Arg	Trp	Phe	Lys	Gly	Ser	Ala	Ser	His	Glu	Tyr	
Arg	Glu	Leu	Asn	Asn	Arg	Ser	Ser	Pro	Arg	Val	Thr	Phe	His	Asp	His	
Thr	Leu	Glu	Phe	Trp	Pro	Val	Glu	Met	Glu	Asp	Glu	Gly	Thr	Tyr	Ile	
Ser	Gln	Val	Gly	Asn	Asp	Arg	Arg	Asn	Trp	Thr	Leu	Asn	Val	Thr	Lys	
Arg	Asn	Lys	His	Ser	Cys	Phe	Ser	Asp	Lys	Leu	Val	Thr	Ser	Arg	Asp	
Val	Glu	Val	Asn	Lys	Ser	Leu	His	Ile	Thr	Cys	Lys	Asn	Pro	Asn	Tyr	
Glu	Glu	Leu	Ile	Gln	Asp	Thr	Trp	Leu	Tyr	Lys	Asn	Cys	Lys	Glu	Ile	
Ser	Lys	Thr	Pro	Arg	Ile	Leu	Lys	Asp	Ala	Glu	Phe	Gly	Asp	Glu	Gly	
Tyr	Tyr	Ser	Cys	Val	Phe	Ser	Val	His	His	Asn	Gly	Thr	Arg	Tyr	Asn	
Ile	Thr	Lys	Thr	Val	Asn	Ile	Thr	Val	Ile	Glu	Gly	Arg	Ser	Lys	Val	
Thr	Pro	Ala	Ile	Leu	Gly	Pro	Lys	Cys	Glu	Lys	Val	Gly	Val	Glu	Leu	
Gly	Lys	Asp	Val	Glu	Leu	Asn	Cys	Ser	Ala	Ser	Leu	Asn	Lys	Asp	Asp	
Leu	Phe	Tyr	Trp	Ser	Ile	Arg	Lys	Glu	Asp	Ser	Ser	Asp	Pro	Asn	Val	
Gln	Glu	Asp	Arg	Lys	Glu	Thr	Thr	Thr	Trp	Ile	Ser	Glu	Gly	Lys	Leu	
His	Ala	Ser	Lys	Ile	Leu	Arg	Phe	Gln	Lys	Ile	Thr	Glu	Asn	Tyr	Leu	
Asn	Val	Leu	Tyr	Asn	Cys	Thr	Val	Ala	Asn	Glu	Glu	Ala	Ile	Asp	Thr	
Lys	Ser	Phe	Val	Leu	Val	Arg	Lys	Glu	Ile	Pro	Asp	Ile	Pro	Gly	His	
Val	Phe	Thr	Gly	Gly	Val	Thr	Val	Leu	Val	Leu	Ala	Ser	Val	Ala	Ala	
Val	Cys	Ile	Val	Ile	Leu	Cys	Val	Ile	Tyr	Lys	Val	Asp	Leu	Val	Leu	
Phe	Tyr	Arg	Arg	Ile	Ala	Glu	Arg	Asp	Glu	Thr	Leu	Thr	Asp	Gly	Lys	
Thr	Tyr	Asp	Ala	Phe	Val	Ser	Tyr	Leu	Lys	Glu	Cys	His	Pro	Glu	Asn	
Lys	Glu	Glu	Tyr	Thr	Phe	Ala	Val	Glu	Thr	Leu	Pro	Arg	Val	Leu	Glu	
Lys	Gln	Phe	Gly	Tyr	Lys	Leu	Cys	Ile	Phe	Glu	Arg	Asp	Val	Val	Pro	

[illegible]

(23) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

25	Glu 1	Ser	Cys	Thr	Ser 5	Arg	Pro	His	Ile	Thr 10	Val	Val	Glu	Gly	Glu 15	Pro
	Phe	Tyr	Leu	Lys 20	His	Cys	Ser	Cys	Ser 25	Leu	Ala	His	Glu	Ile 30	Glu	Thr
	Thr	Thr	Lys 35	Ser	Trp	Tyr	Lys	Ser 40	Ser	Gly	Ser	Gln	Glu 45	His	Val	Glu
30	Leu	Asn 50	Pro	Arg	Ser	Ser	Ser 55	Arg	Ile	Ala	Leu	His 60	Asp	Cys	Val	Leu
	Glu 65	Phe	Trp	Pro	Val	Glu 70	Leu	Asn	Asp	Thr	Gly 75	Ser	Tyr	Phe	Phe	Gln 80
	Met	Lys	Asn	Tyr	Thr 85	Gln	Lys	Trp	Lys	Leu 90	Asn	Val	Ile	Arg	Arg 95	Asn
35	Lys	His	Ser	Cys 100	Phe	Thr	Glu	Arg	Gln 105	Val	Thr	Ser	Lys	Ile 110	Val	Glu
	Val	Lys	Lys 115	Phe	Phe	Gln	Ile	Thr 120	Cys	Glu	Asn	Ser	Tyr 125	Tyr	Gln	Thr
	Leu 130	Val	Asn	Ser	Thr	Ser	Leu 135	Tyr	Lys	Asn	Cys	Lys 140	Lys	Leu	Leu	Leu
40	Glu 145	Asn	Asn	Lys	Asn	Pro 150	Thr	Ile	Lys	Lys	Asn 155	Ala	Glu	Phe	Glu	Asp 160
	Gln	Gly	Tyr	Tyr	Ser 165	Cys	Val	His	Phe	Leu 170	His	His	Asn	Gly	Lys 175	Leu
	Phe	Asn	Ile	Thr 180	Lys	Thr	Phe	Asn 185	Ile	Thr	Ile	Val	Glu	Asp 190	Arg	Ser
45	Asn	Ile 195	Val	Pro	Val	Leu	Leu	Gly 200	Pro	Lys	Leu	Asn 205	His	Val	Ala	Val
	Glu 210	Leu	Gly	Lys	Asn	Val	Arg 215	Leu	Asn	Cys	Ser	Ala 220	Leu	Leu	Asn	Glu
	Glu 225	Asp	Val	Ile	Tyr	Trp 230	Met	Phe	Gly	Glu	Glu	Asn 235	Gly	Ser	Asp	Pro 240
50	Asn	Ile	His	Glu	Glu 245	Lys	Glu	Met	Arg	Ile 250	Met	Thr	Pro	Glu	Gly 255	Lys
	Trp	His	Ala	Ser 260	Lys	Val	Leu	Arg	Ile 265	Glu	Asn	Ile	Gly	Glu	Ser	Asn
	Leu	Asn	Val	Leu	Tyr	Asn	Cys	Thr	Val	Ala	Ser	Thr	Gly	Gly	Thr	Asp

275 280 285
 Thr Lys Ser Phe Ile Leu Val Arg Lys Asp Met Ala Asp Ile Pro Gly
 290 295 300
 His Val Phe Thr Arg
 305

(24) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:207

(B) TYPE:amino acid

(D) TOPOLOGY:linear

(ii) MOLECULE TYPE:peptide

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:23:

15
 1 5 10 15
 Glu Ser Cys Thr Ser Arg Pro His Ile Thr Val Val Glu Gly Glu Pro
 Phe Tyr Leu Lys His Cys Ser Cys Ser Leu Ala His Glu Ile Glu Thr
 20
 20 25 30
 Thr Thr Lys Ser Trp Tyr Lys Ser Ser Gly Ser Gln Glu His Val Glu
 Leu Asn Pro Arg Ser Ser Ser Arg Ile Ala Leu His Asp Cys Val Leu
 25
 30 35 40 45
 Glu Phe Trp Pro Val Glu Leu Asn Asp Thr Gly Ser Tyr Phe Phe Gln
 Met Lys Asn Tyr Thr Gln Lys Trp Lys Leu Asn Val Ile Arg Arg Asn
 35
 40 45 50 55
 Lys His Ser Cys Phe Thr Glu Arg Gln Val Thr Ser Lys Ile Val Glu
 Val Lys Lys Phe Phe Gln Ile Thr Cys Glu Asn Ser Tyr Tyr Gln Thr
 45
 50 55 60 65
 Leu Val Asn Ser Thr Ser Leu Tyr Lys Asn Cys Lys Lys Leu Leu Leu
 Glu Asn Asn Lys Asn Pro Thr Ile Lys Lys Asn Ala Glu Phe Glu Asp
 55
 60 65 70 75
 Gln Gly Tyr Tyr Ser Cys Val His Phe Leu His His Asn Gly Lys Leu
 Phe Asn Ile Thr Lys Thr Phe Asn Ile Thr Ile Val Glu Asp Arg Ser
 65
 70 75 80 85
 Asn Ile Val Pro Val Leu Leu Gly Pro Lys Leu Asn His Val Ala
 80
 85 90 95 100
 195 200 205

(25) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:104

(B) TYPE:amino acid

(D) TOPOLOGY:linear

(ii) MOLECULE TYPE:peptide

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:24:

45
 1 5 10 15
 Glu Ser Cys Thr Ser Arg Pro His Ile Thr Val Val Glu Gly Glu Pro
 Phe Tyr Leu Lys His Cys Ser Cys Ser Leu Ala His Glu Ile Glu Thr
 50
 55 60 65
 The Thr Lys Ser Trp Tyr Lys Ser Ser Gly Ser Gln Glu His Val Glu
 Leu Asn Pro Arg Ser Ser Ser Arg Ile Ala Leu His Asp Cys Val Leu
 60
 65 70 75 80
 Glu Phe Trp Pro Val Glu Leu Asn Asp Thr Gly Ser Tyr Phe Phe Gln
 Met Lys Asn Tyr Thr Gln Lys Trp Lys Leu Asn Val Ile Arg Arg Asn
 85 90 95

Lys His Ser Cys Phe Thr Glu Arg
100

(26) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:307

(B) TYPE:amino acid

(D) TOPOLOGY:linear

(ii) MOLECULE TYPE:peptide

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:25:

Ser	Lys	Ser	Cys	Ile	His	Arg	Ser	Gln	Ile	His	Val	Val	Glu	Gly	Glu
1				5					10					15	
Pro	Phe	Tyr	Leu	Lys	Pro	Cys	Gly	Ile	Ser	Ala	Pro	Val	His	Arg	Asn
			20					25					30		
Glu	Thr	Ala	Thr	Met	Arg	Trp	Phe	Lys	Gly	Ser	Ala	Ser	His	Glu	Tyr
		35					40					45			
Arg	Glu	Leu	Asn	Asn	Arg	Ser	Ser	Pro	Arg	Val	Thr	Phe	His	Asp	His
	50					55					60				
Thr	Leu	Glu	Phe	Trp	Pro	Val	Glu	Met	Glu	Asp	Glu	Gly	Thr	Tyr	Ile
	65				70				75					80	
Ser	Gln	Val	Gly	Asn	Asp	Arg	Arg	Asn	Trp	Thr	Leu	Asn	Val	Thr	Lys
			85					90						95	
Arg	Asn	Lys	His	Ser	Cys	Phe	Ser	Asp	Lys	Leu	Val	Thr	Ser	Arg	Asp
			100					105					110		
Val	Glu	Val	Asn	Lys	Ser	Leu	His	Ile	Thr	Cys	Lys	Asn	Pro	Asn	Tyr
		115					120					125			
Glu	Glu	Leu	Ile	Gln	Asp	Thr	Trp	Leu	Tyr	Lys	Asn	Cys	Lys	Glu	Ile
	130					135					140				
Ser	Lys	Thr	Pro	Arg	Ile	Leu	Lys	Asp	Ala	Glu	Phe	Gly	Asp	Glu	Gly
145					150					155				160	
Tyr	Tyr	Ser	Cys	Val	Phe	Ser	Val	His	His	Asn	Gly	Thr	Arg	Tyr	Asn
			165					170					175		
Ile	Thr	Lys	Thr	Val	Asn	Ile	Thr	Val	Ile	Glu	Gly	Arg	Ser	Lys	Val
			180					185					190		
Thr	Pro	Ala	Ile	Leu	Gly	Pro	Lys	Cys	Glu	Lys	Val	Gly	Val	Glu	Leu
		195					200					205			
Gly	Lys	Asp	Val	Glu	Leu	Asn	Cys	Ser	Ala	Ser	Leu	Asn	Lys	Asp	Asp
	210					215					220				
Leu	Phe	Tyr	Trp	Ser	Ile	Arg	Lys	Glu	Asp	Ser	Ser	Asp	Pro	Asn	Val
225					230					235				240	
Gln	Glu	Asp	Arg	Lys	Glu	Thr	Thr	Thr	Trp	Ile	Ser	Glu	Gly	Lys	Leu
			245						250				255		
His	Ala	Ser	Lys	Ile	Leu	Arg	Phe	Gln	Lys	Ile	Thr	Glu	Asn	Tyr	Leu
			260					265					270		
Asn	Val	Leu	Tyr	Asn	Cys	Thr	Val	Ala	Asn	Glu	Glu	Ala	Ile	Asp	Thr
		275					280					285			
Lys	Ser	Phe	Val	Leu	Val	Arg	Lys	Glu	Ile	Pro	Asp	Ile	Pro	Gly	His
	290					295					300				
Val	Phe	Thr													
305															

(27) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:157

(B) TYPE:amino acid

(D) TOPOLOGY:linear

(ii) MOLECULE TYPE:peptide

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:26:

Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn

1				5					10					15		
Asp	Gln	Val	Leu	Phe	Ile	Asp	Gln	Gly	Asn	Arg	Pro	Leu	Phe	Glu	Asp	
			20					25					30			
Met	Thr	Asp	Ser	Asp	Cys	Arg	Asp	Asn	Ala	Pro	Arg	Thr	Ile	Phe	Ile	
		35					40					45				
Ile	Ser	Met	Tyr	Lys	Asp	Ser	Gln	Pro	Arg	Gly	Met	Ala	Val	Thr	Ile	
	50					55					60					
Ser	Val	Lys	Cys	Glu	Lys	Ile	Ser	Xaa	Leu	Ser	Cys	Glu	Asn	Lys	Ile	
	65				70					75						
Ile	Ser	Phe	Lys	Glu	Met	Asn	Pro	Pro	Asp	Asn	Ile	Lys	Asp	Thr	Lys	
				85					90					95		
Ser	Asp	Ile	Ile	Phe	Phe	Gln	Arg	Ser	Val	Pro	Gly	His	Asp	Asn	Lys	
			100					105					110			
Met	Gln	Phe	Glu	Ser	Ser	Ser	Tyr	Glu	Gly	Tyr	Phe	Leu	Ala	Cys	Glu	
		115					120					125				
Lys	Glu	Arg	Asp	Leu	Phe	Lys	Leu	Ile	Leu	Lys	Lys	Glu	Asp	Glu	Leu	
	130					135					140					
Gly	Asp	Arg	Ser	Ile	Met	Phe	Thr	Val	Gln	Asn	Glu	Asp				
145					150					155						

(28) INFORMATION FOR SEQ ID NO:27:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH:157
 (B) TYPE:amino acid
 (D) TOPOLOGY:linear
 (ii) MOLECULE TYPE:peptide
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:27:

Asn 1	Phe	Gly	Arg	Leu 5	His	Cys	Thr	Thr	Ala 10	Val	Ile	Arg	Asn	Ile 15	Asn
Asp	Gln	Val	Leu 20	Phe	Val	Asp	Lys	Arg 25	Gln	Pro	Val	Phe	Glu 30	Asp	Met
Thr	Asp	Ile 35	Asp	Gln	Ser	Ala	Ser 40	Glu	Pro	Gln	Thr	Arg 45	Leu	Ile	Ile
Tyr	Met 50	Tyr	Lys	Asp	Ser	Glu 55	Val	Arg	Gly	Leu	Ala 60	Val	Thr	Leu	Ser
Val 65	Lys	Asp	Ser	Lys	Xaa 70	Ser	Thr	Leu	Ser	Cys 75	Lys	Asn	Lys	Ile 80	Ile
Ser	Phe	Glu	Glu 85	Met	Asp	Pro	Pro	Glu	Asn 90	Ile	Asp	Asp	Ile	Gln 95	Ser
Asp	Leu	Ile	Phe 100	Phe	Gln	Lys	Arg	Val 105	Pro	Gly	His	Asn	Lys 110	Met	Glu
Phe	Glu	Ser 115	Ser	Leu	Tyr	Glu	Gly 120	His	Phe	Leu	Ala	Cys 125	Gln	Lys	Glu
Asp	Asp 130	Ala	Phe	Lys	Leu	Ile 135	Leu	Lys	Lys	Lys	Asp 140	Glu	Asn	Gly	Asp
Lys 145	Ser	Val	Met	Phe	Thr 150	Leu	Thr	Asn	Leu	His 155	Gln	Ser			

Claims

- 50 1. A polypeptide as interleukin-18 receptor, which is obtainable through gene expression.
2. The polypeptide of claim 1, which is obtainable by bringing into expression a human or mouse gene in a host of animal, plant or microbe origin.
- 55 3. The polypeptide of claim 1, wherein said gene contains a part or whole of the nucleotide sequence of SEQ ID NO:1 or 2.
4. The polypeptide of claim 1, wherein said gene contains the nucleotide sequence of SEQ ID NO:3 or 4.

5. The polypeptide of claim 1, wherein said gene contains either nucleotide sequence of SEQ ID NOs:5 to 11.
6. The polypeptide of claim 1, which contains one or more amino acid sequences of SEQ ID NOs:12 to 19.
- 5 7. The polypeptide of claim 1, which contains a part or whole of the nucleotide sequence of SEQ ID NO:20 or 21.
8. The polypeptide of claim 1, which contains either amino acid sequence of SEQ ID NOs:22 to 25.
9. An agent for interleukin-18 receptor susceptible diseases, which contains as effective ingredient the polypeptide of
10 claim 1.
10. The agent of claim 9, which contains as stabilizer a protein, saccharide and/or buffer.
11. An anti-autoimmune disease agent in accordance with claim 9.
- 15 12. An immunosuppressant in accordance with claim 9.
13. A DNA which encodes the polypeptide of claim 1.
- 20 14. The DNA of claim 13, which originates from human or mouse.
15. The DNA of claim 13, which contains a part or whole of either nucleotide sequence of SEQ ID NO:1, SEQ ID NO:2
or their complementary sequence.
- 25 16. The DNA of claim 13, which contains either nucleotide sequence of SEQ ID NO:3, SEQ ID NO:4 or their comple-
mentary sequence.
17. The DNA of claim 13, which contains either nucleotide sequence of SEQ ID NO: 5, SEQ ID: 6, SEQ ID NO: 7, SEQ
ID NO:8, SEQ ID NO:9, SEQ ID NO: 10, SEQ ID NO: 11 or their complementary sequence.
- 30 18. The DNA of claim 13, wherein, based on the degeneracy of genetic codes, one or more nucleotides are replaced
with different nucleotides while conserving the amino acid sequence.
19. The DNA of claim 13, which is placed in an autonomously replicable vector.
- 35 20. The DNA of claim 13, which is placed in a host of animal, plant or microbe origin.
21. A process to prepare polypeptide, comprising bringing into expression a DNA which encodes the polypeptide of
claim 1; and collecting the resultant polypeptide.
- 40 22. The process of claim 21, wherein the resultant polypeptide is collected through a step which includes salting out,
dialysis, filtration, concentration, fractional precipitation, ion-exchange chromatography, gel filtration chromatogra-
phy, adsorption chromatography, isoelectric focusing chromatography, hydrophobic chromatography, reversed
phase chromatography, affinity chromatography, gel electrophoresis and/or isoelectric focusing gel electrophoresis.
- 45 23. The process of claim 21, wherein the resultant polypeptide is collected through a step which includes immunoaffin-
ity chromatography using monoclonal antibody.
24. A agent to neutralize interleukin-18, which contains as effective ingredient the polypeptide of claim 1.
- 50 25. A method to neutralize interleukin-18, characterized by allowing the polypeptide of claim 1 to act on interleukin-18.

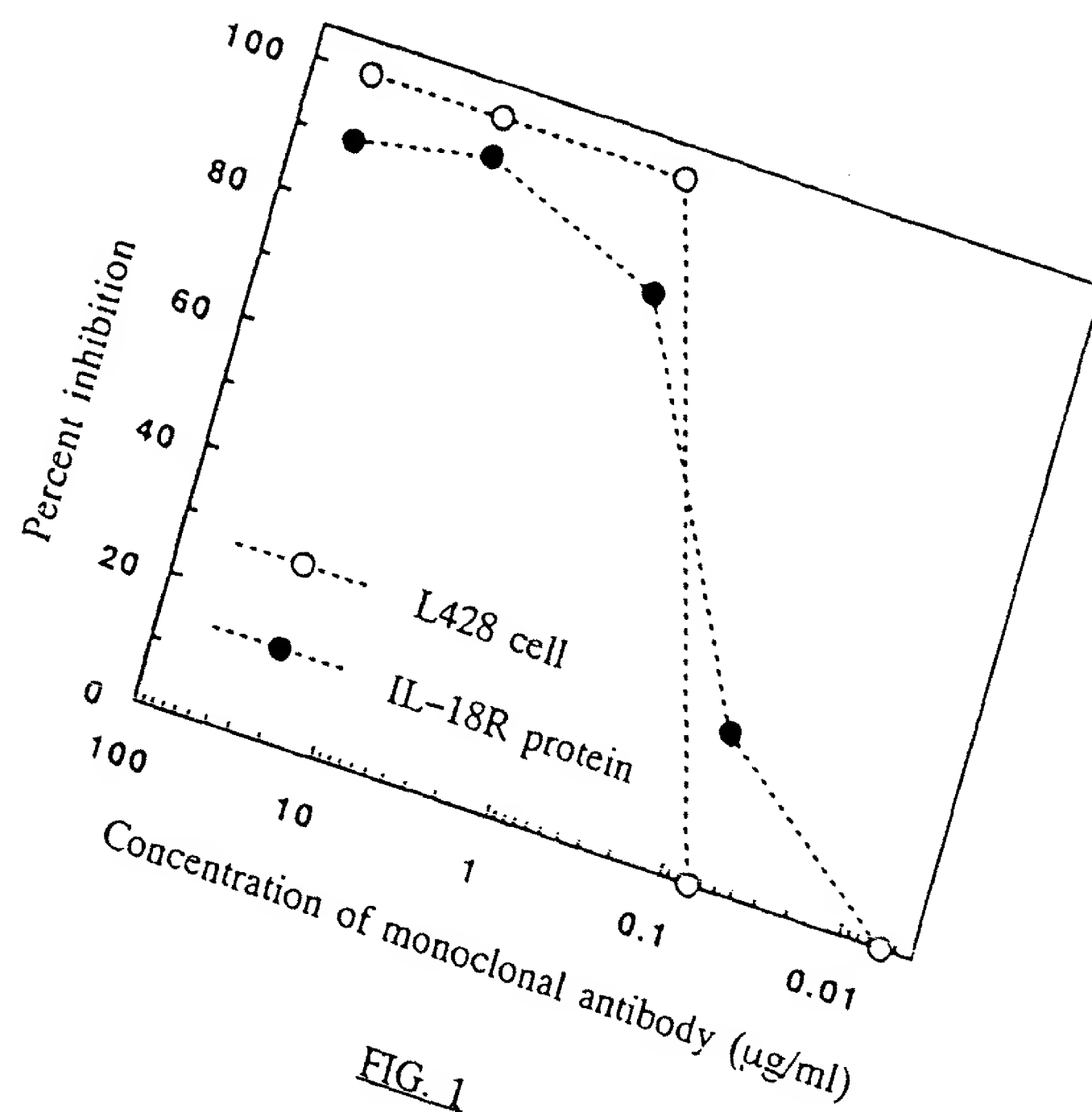
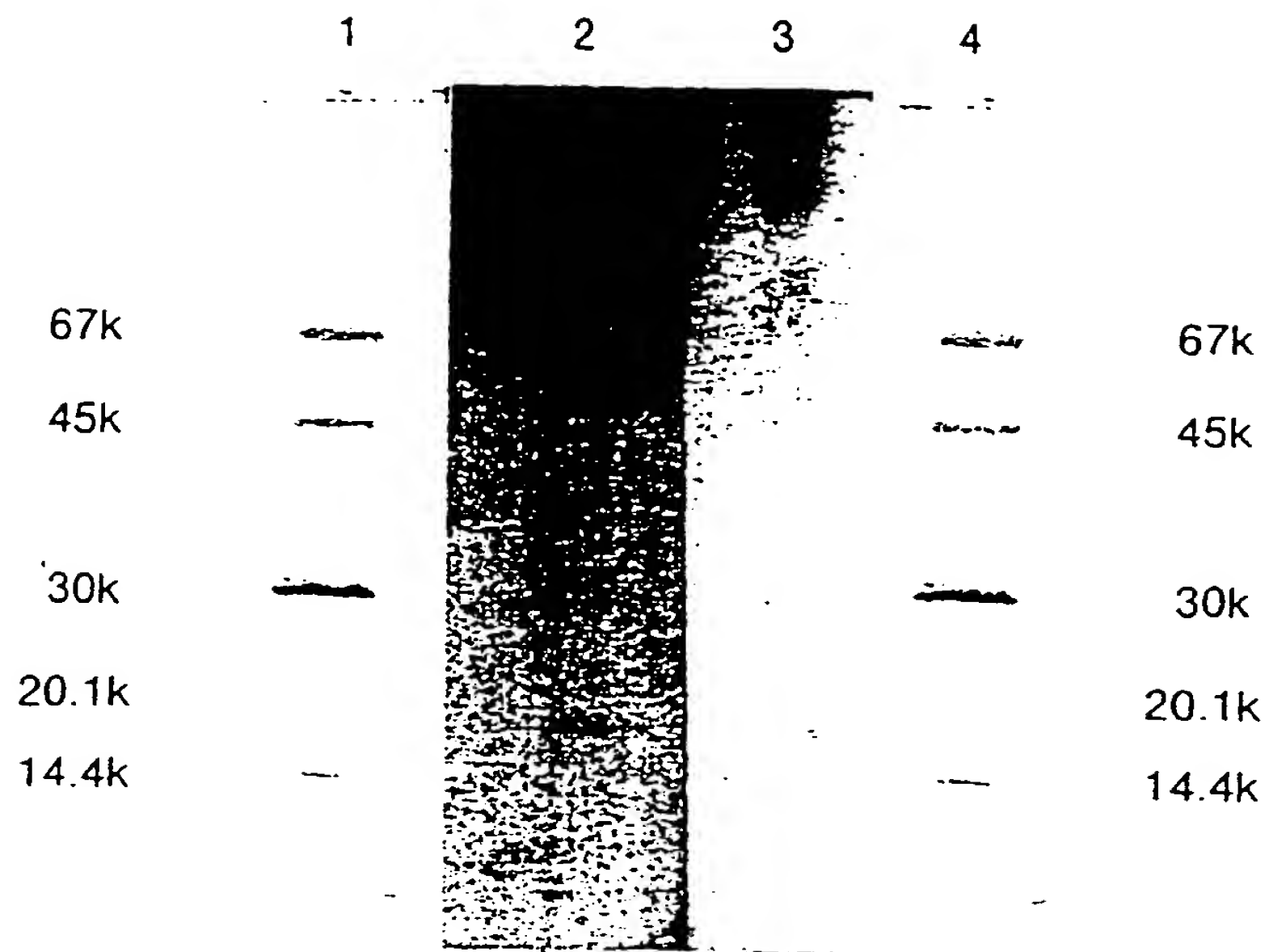


FIG. 1



Lane 1 : Molecular weight markers
 Lane 2 : Sample (with monoclonal antibody)
 Lane 3 : Sample (without monoclonal antibody)
 Lane 4 : Molecular weight markers

FIG. 2

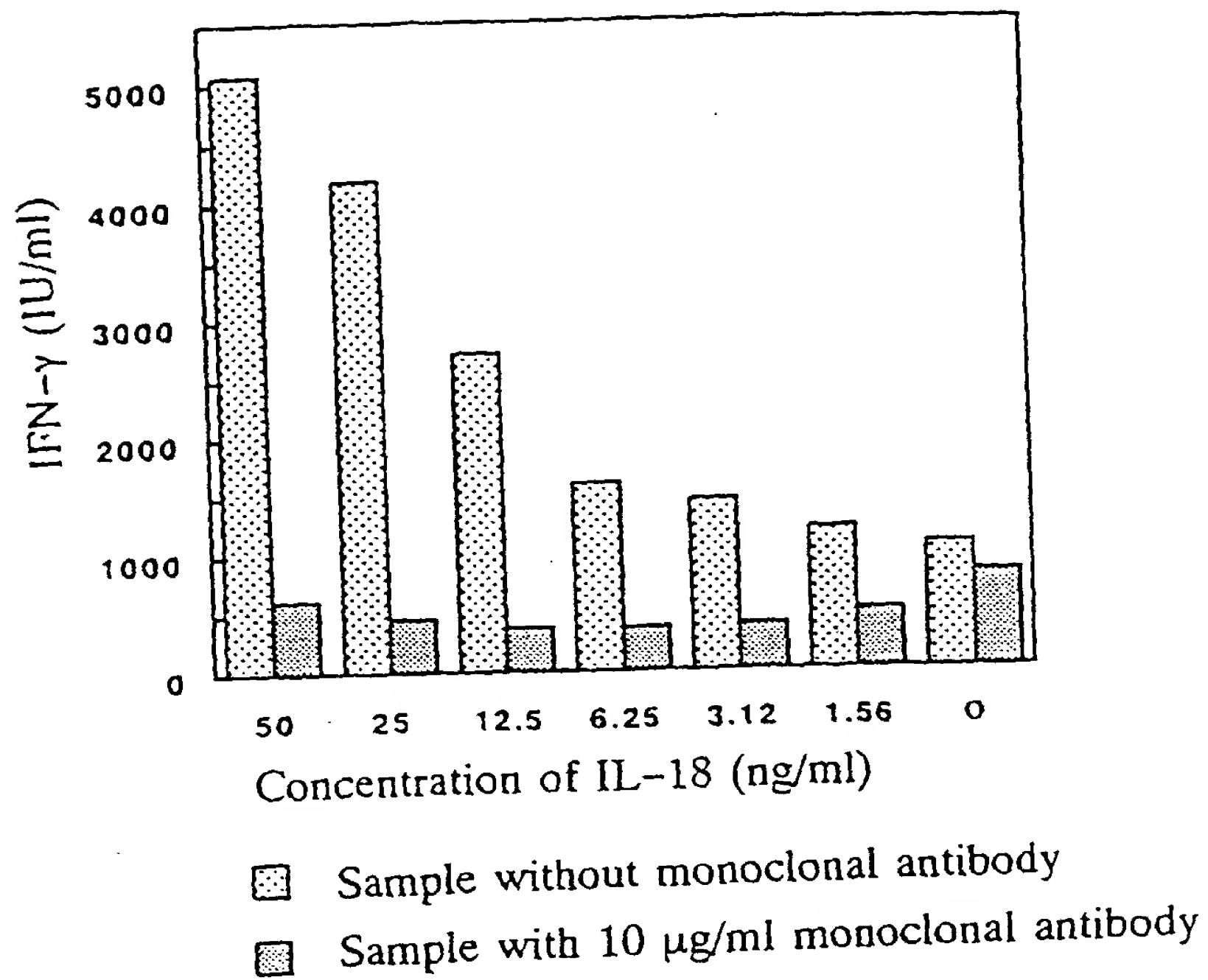


FIG. 3

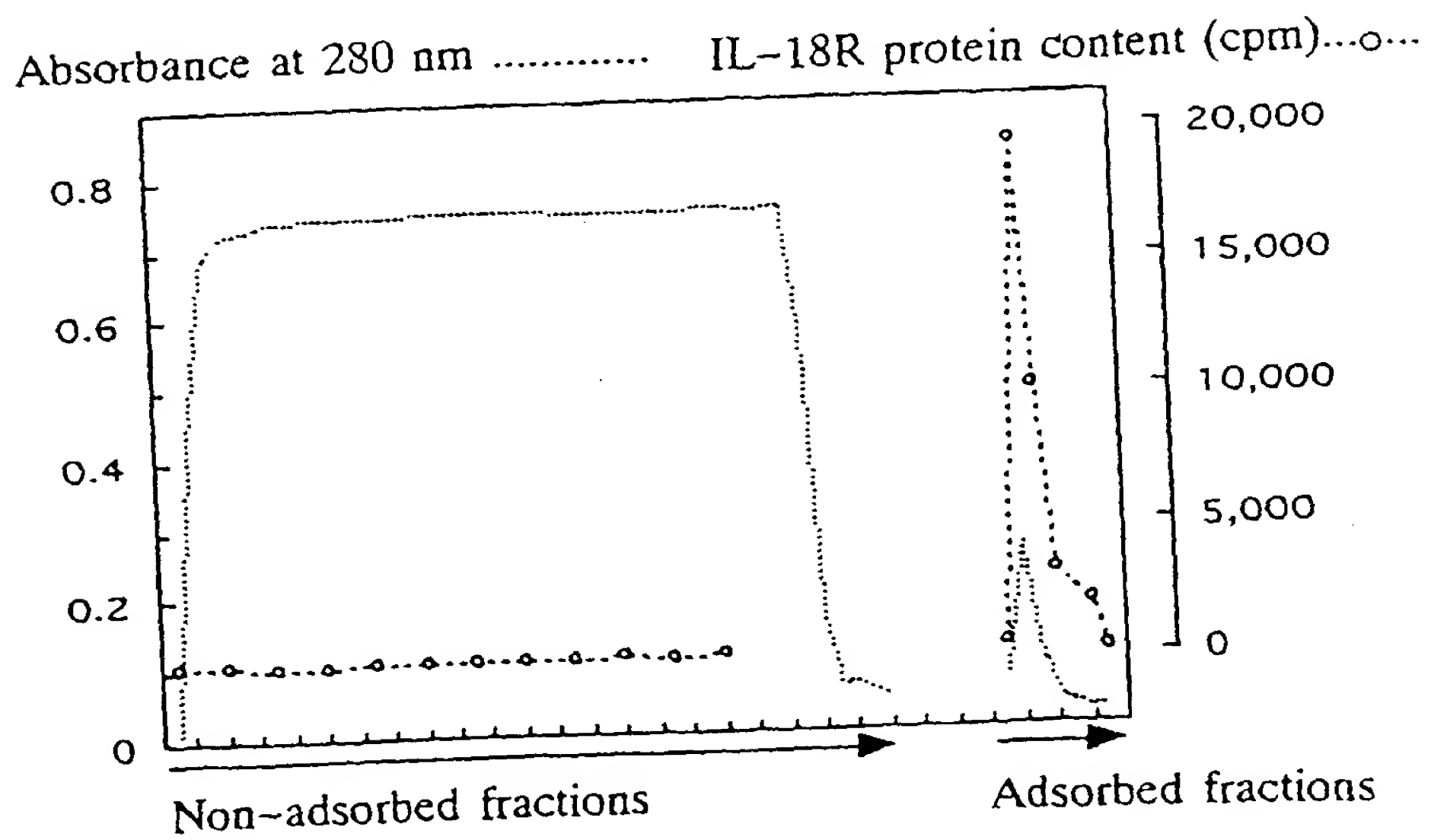


FIG. 4

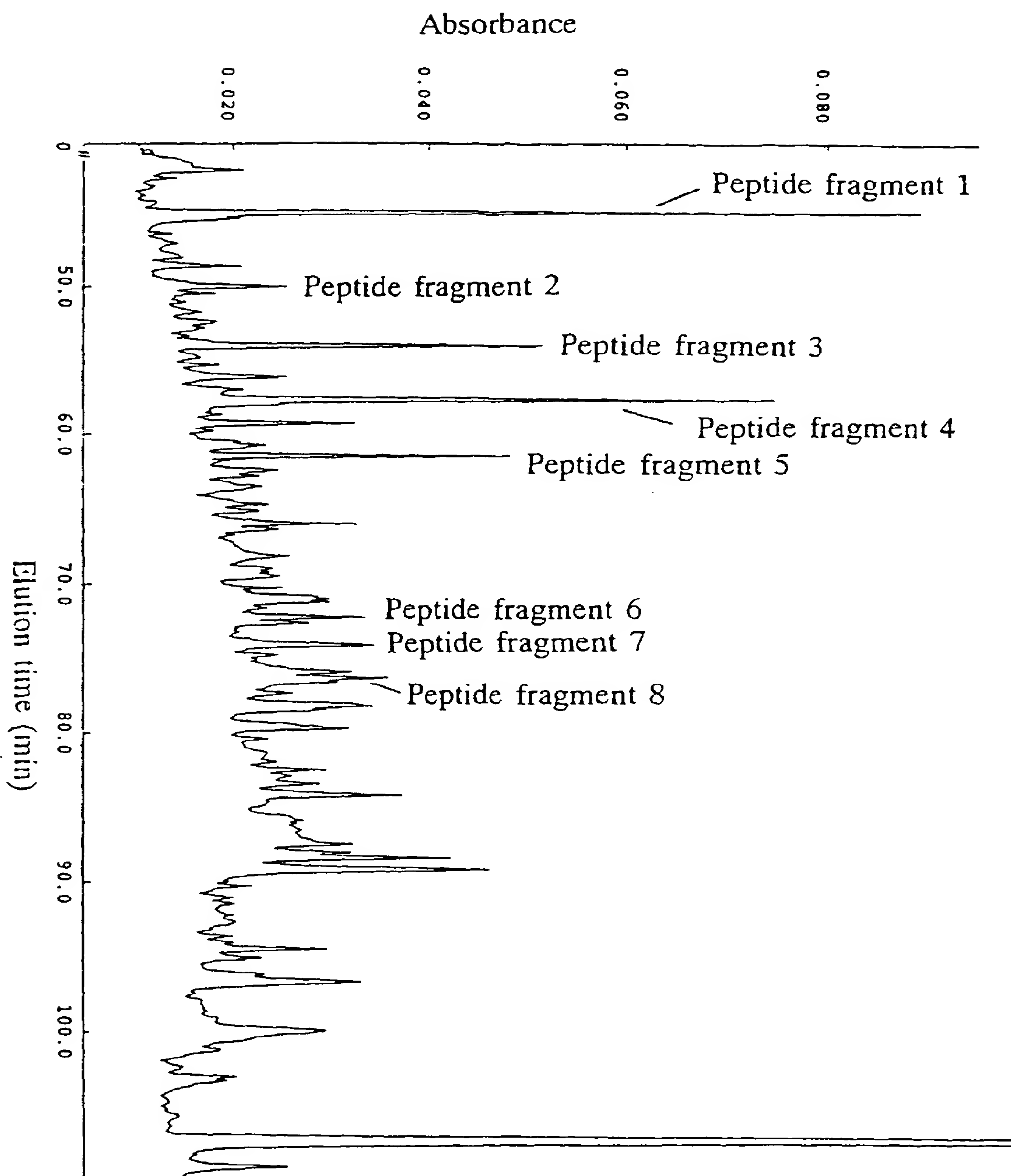


FIG. 5

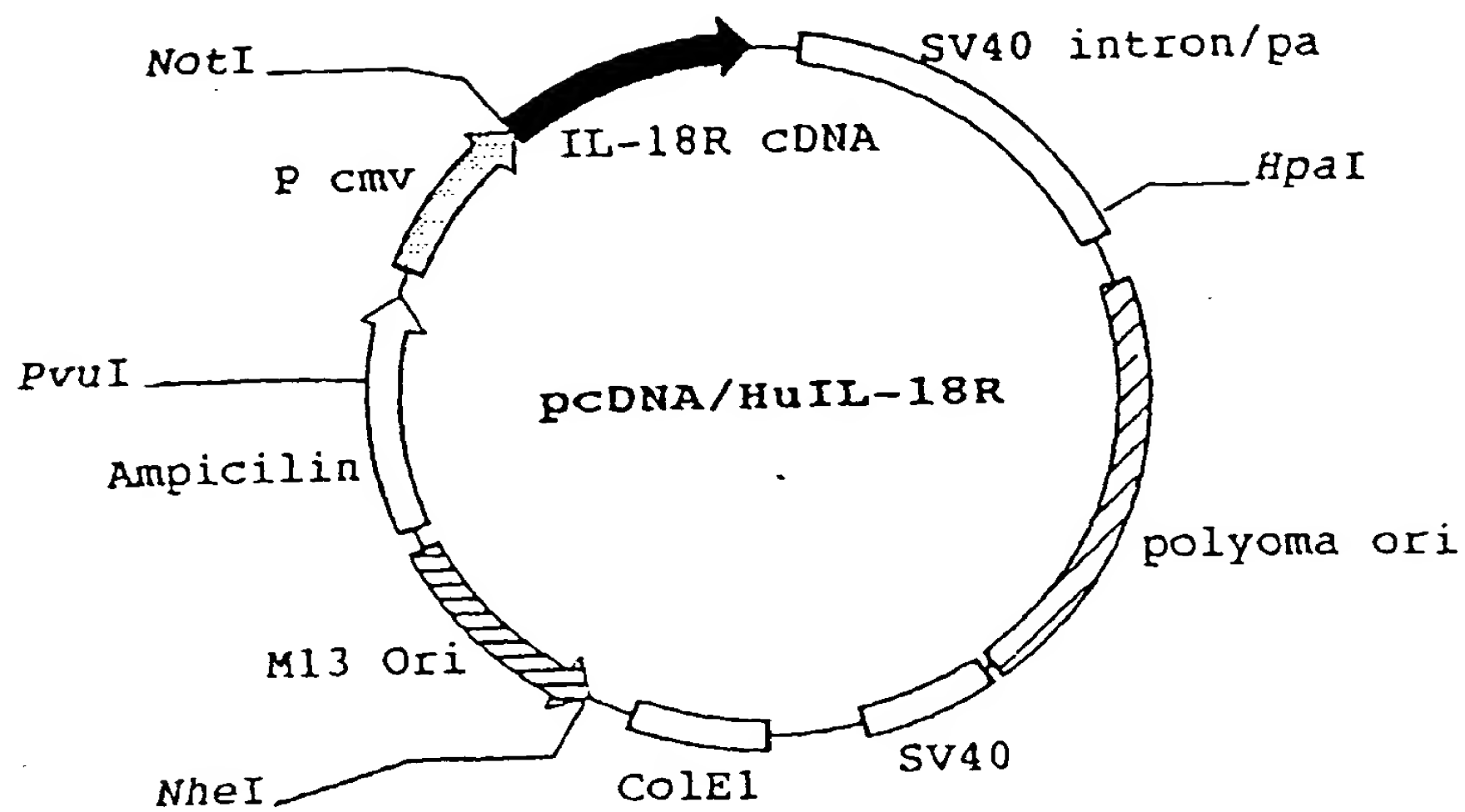


FIG. 6

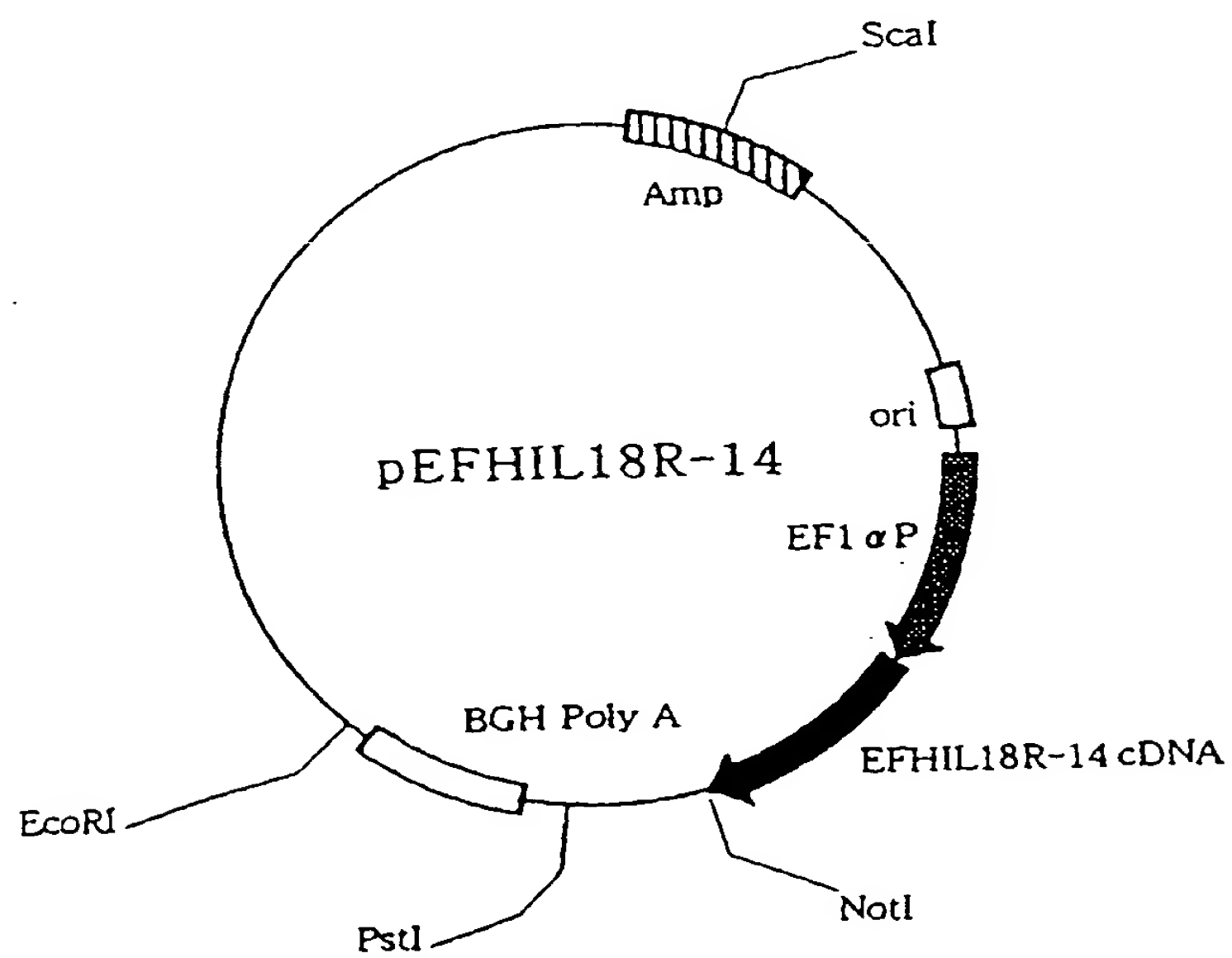


FIG. 7

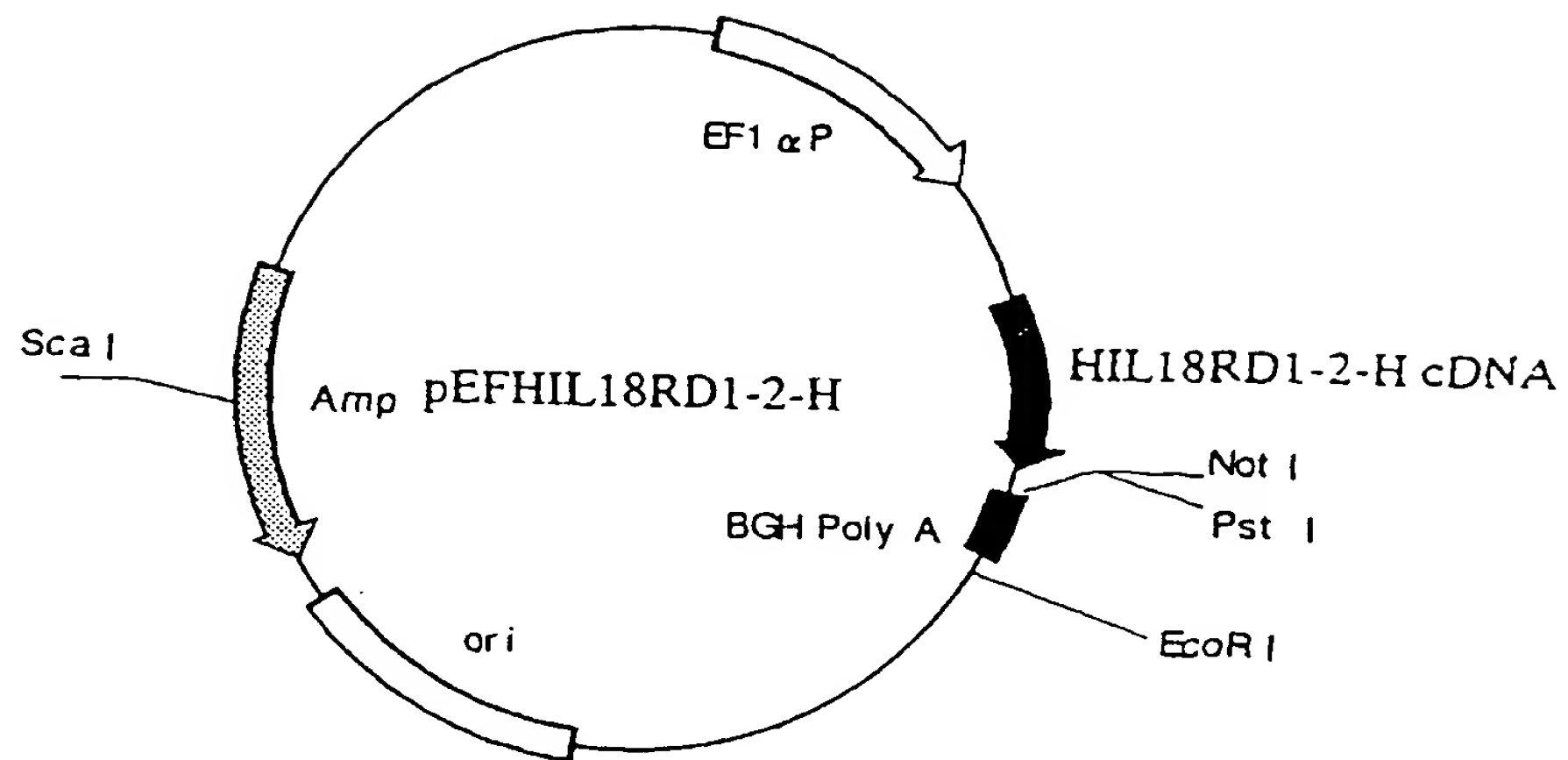


FIG. 8

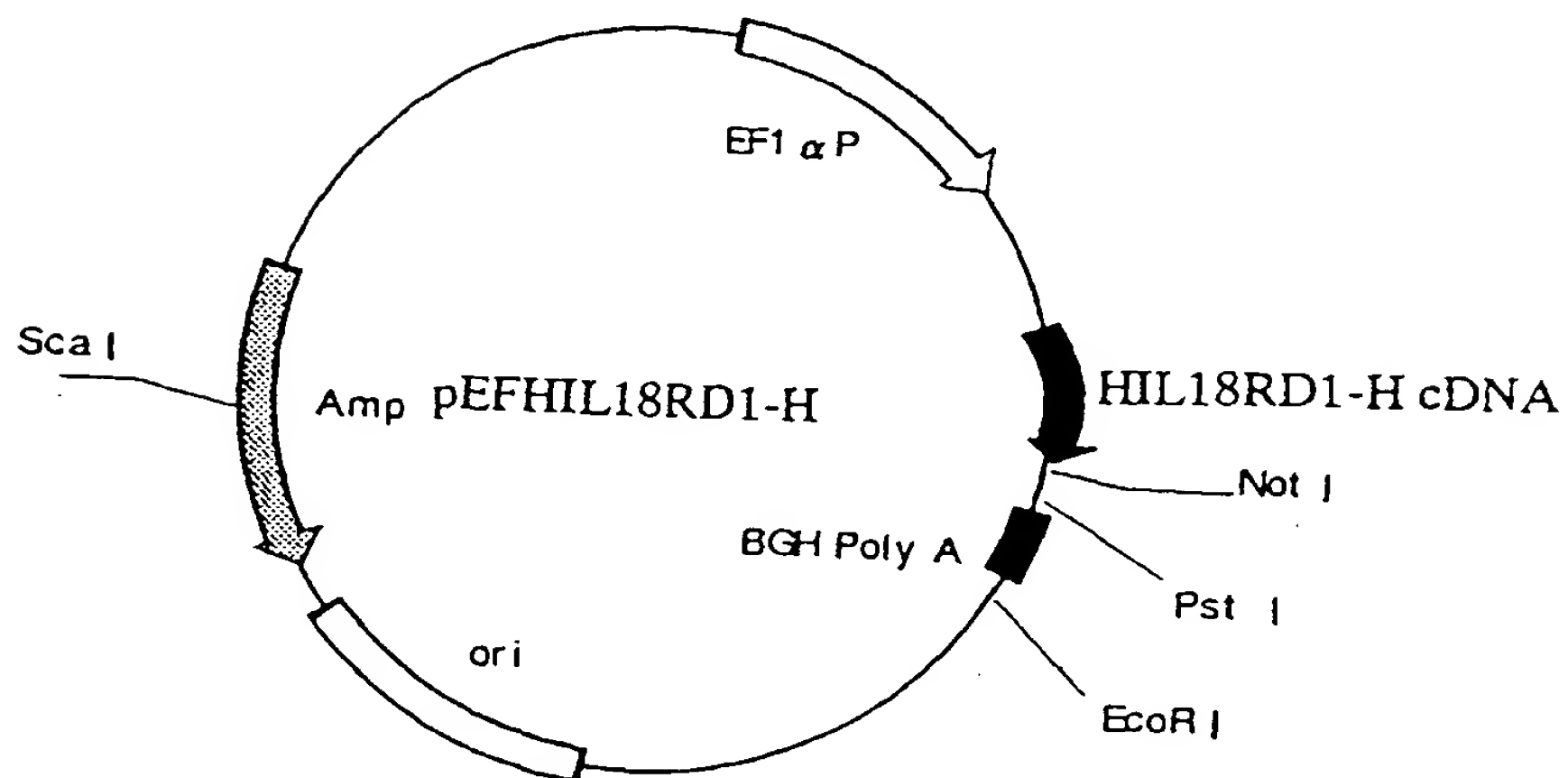


FIG. 9

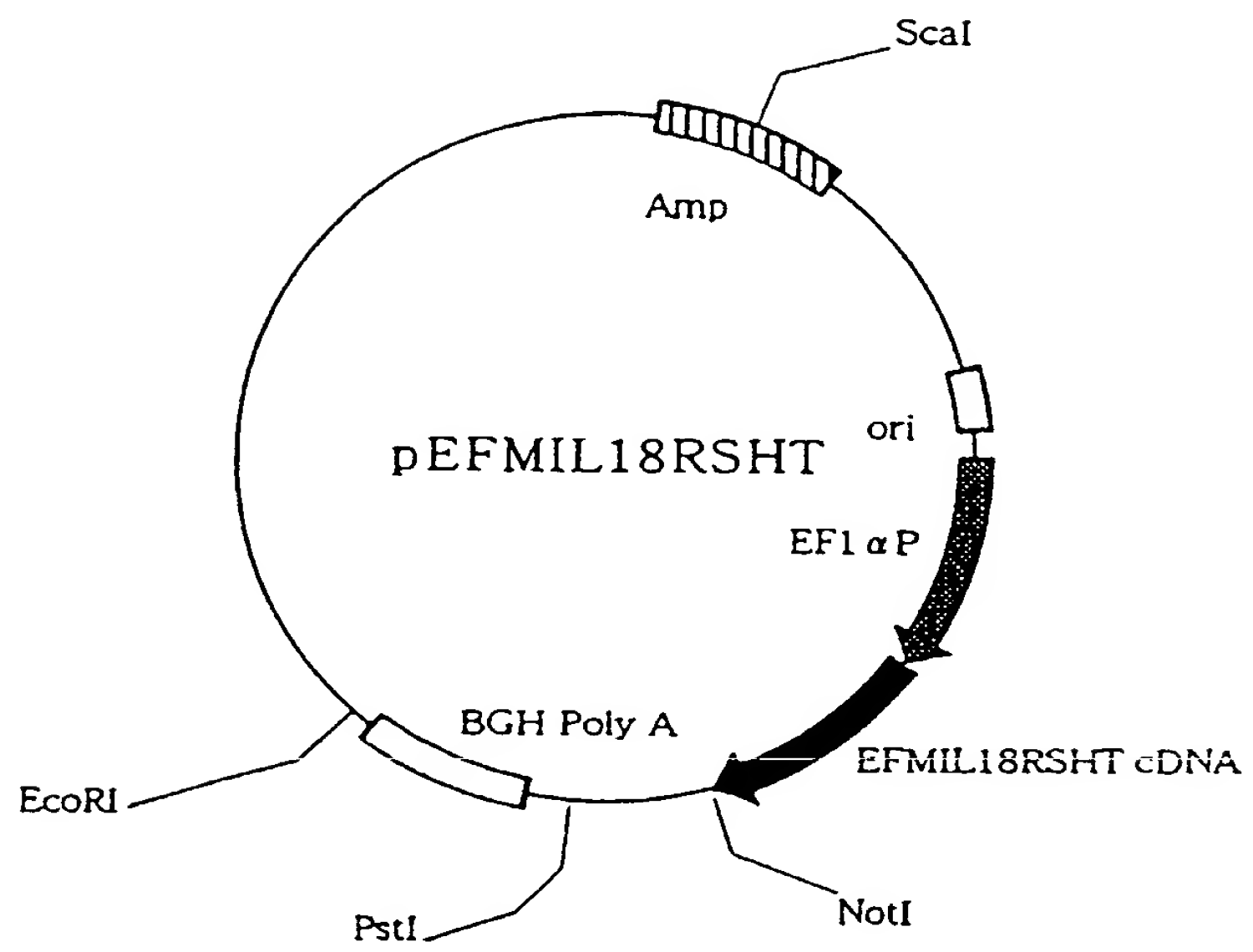


FIG. 10



European Patent
Office

EUROPEAN SEARCH REPORT

Application Number
EP 97 31 0517

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
X	PARNET, P. ET AL.: "IL-1Rrp is a novel receptor-like molecule similar to the type I interleukin-1 receptor and its homologs T1/ST2 and IL-1R AcP" J. BIOL. CHEM., 271(8), 3967-70, 23 February 1996, XP002059933 * figure 1 *	1-11,27	C07K14/715 A61K38/17 A61K39/00
P,X	WO 97 31010 A (IMMUNEX CORP) 28 August 1997 * the whole document *	1-28	
			TECHNICAL FIELDS SEARCHED (Int.Cl.6)
			C07K A61K
The present search report has been drawn up for all claims			
Place of search MUNICH		Date of completion of the search 25 March 1998	Examiner Chakravarty, A
<p>CATEGORY OF CITED DOCUMENTS</p> <p>X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document</p> <p>T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document</p>			

EPF FORM 1503 03 92 (P04C01)

